The Utility of Cladistic Analysis of Nonmetric Skeletal Traits for Biodistance Analysis

by

James Christopher Reed

B.A., Mississippi State University, 1994

M.A., University of South Carolina, 1998

Submitted to the Graduate Faculty of

Arts and Sciences in partial fulfillment

of the requirements for the degree of

Doctor of Philosophy

University of Pittsburgh

2006

UNIVERSITY OF PITTSBURGH

Faculty of Arts and Sciences

This dissertation was presented

by

James Christopher Reed

It was defended on

April 17, 2006

and approved by

Dr. Michael I. Siegel, Professor, Department of Anthropology

Dr. Mark P. Mooney, Professor, Department of Oral Medicine and Pathology

Dr. Marc P. Bermann, Associate Professor, Department of Anthropology

Dr. Jeffrey H. Schwartz, Professor, Department of Anthropology
Dissertation Director

The Utility of Cladistic Analysis of Nonmetric Skeletal Traits for Biodistance Analysis

James Christopher Reed, PhD

University of Pittsburgh, 2006

A significant focus of bioarchaeology is biodistance analysis, which seeks to determine the biological affinities of human groups and to support arguments about prehistoric and historic cultural topics, such as migration, marriage, and residential patterns. Although genetic comparisons are becoming more common, metric and nonmetric skeletal traits remain the primary source of information on human populations.

Biodistance analysis is grounded theoretically and methodologically in phenetics, which is an approach developed by systematists to group organisms on the basis of overall similarity. However, while phenetics was adopted by physical anthropologists and bioarchaeologists as the foundation of biodistance analysis, systematists have long since moved away from phenetic approaches for determining relatedness to hypothetico-deductively based cladistic analyses. It is time for physical anthropologists and bioarchaeologists engaged in biodistance analysis do so as well.

It is perhaps an irony that biodistance analysis, which seeks to delineate the biological relationships of group, begins by defining the groups (samples) on the basis of archaeological, cultural, or linguistic information prior to any morphological/biological comparison. However, the delineation and comparison of groups should be based from the beginning on the biology (morphology) of individuals and then of groups and, more specifically, on unique biological features, not cultural or linguistic criteria. A cladistic analysis can provide a biologically based delineation of groups.

In this study I investigate whether unique, nonmetric characters can be delineated for small groups such as those traditionally the focus of biodistance analysis and, thus,

whether cladistic analysis is an appropriate substitute for the phenetic approach in biodistance analysis. Four samples of skeletal material were examined. One, the Spitalfields collection, consists of burials of individuals whose familial relationships are well documented. The other samples are undocumented and compared to the Spitalfields sample in an attempt to delineate unique characters that might define groups.

The result was that no unique characters could be delineated, which means that cladistic analysis, while perhaps applicable to study of higher-level groups within the species, fails at the population level. Consequently, while unsatisfactory, biodistance analysis must continue to rely on abiological criteria for defining populations.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

PREFACE

The idea for this project came from my initial reading of the book *Skeleton Keys* by Dr. Jeffrey Schwartz. The discussion of the analysis of nonmetric and metric characters in order to compare the similarities and differences of different skeletal samples to determine relatedness made me wonder, why do we do this biodistance analysis this way? I also wondered if this sort of analysis is genuinely effective. Ultimately, I came to ask the question, if someone brought a single human cranium or another bone without provenance to an osteologist, would that osteologist be able to say, without reservation, to what group that individual belonged?

I quickly realized that without adequate documentation about from where the cranium originated or samples with which to compare it, identification with any group in the world would be near to impossible. I then began to ask questions about why we as osteologists/bioarchaeologists do what we do during an analysis. As I looked more closely at the method and theory behind biodistance analysis, I questioned its effectiveness. Just as osteologists had looked to systematics for the currently-used phenetic methods of biodistance, I looked to systematics to see if cladistic (hypothetico-deductive) methods could be more effectively used. This project is the result of the desire to determine if a more effective means of biodistance analysis could be developed by using cladistics.

The support of many people was vital to the completion of this dissertation. First, my academic advisor Dr. Jeffrey Schwartz, who has guided my academic and intellectual training for these last several years, deserves the highest order of gratitude for his direction and patience seeing me through to the end of this project. I thank Dr. Michael

I. Siegel, Dr. Mark P. Mooney, and Dr. Marc P. Bermann for their support as members of my dissertation committee and their insight into how I could clarify some of the more dense portions of the writing and keeping me focused on answering the questions asked.

Several people and institutions made this project possible by helping with and allowing access to collections of human skeletal material. I'd like to thank Dr. Louise Humphrey, Prof. Chris Stringer, Dr. Christophe Soligo, and Robert Kruszynski of the Department of Paleontology, Natural History Museum, London, who not only provided access to the Spitalfields Collection, but made me feel so much at home during my stay in London. Thanks in particular go to Louise and Christophe for making my stay so much fun. All pictures of specimens from the Spitalfields Collection, while taken by the author, are courtesy of the Natural History Museum, London.

I would also like to thank Dr. Keith Jacobi of the Department of Anthropology, University of Alabama for allowing me access to the Perry Site burial sample. Keith also generously shared his Alabama basketball tickets and gave me a copy of a book which ended a long search, for which I am very grateful. Dr. David Hunt, Department of Anthropology, National Museum of Natural History (Smithsonian) graciously allowed me to examine the specimens of the Terry Collection. Sue McLaren, Section of Mammals, Carnegie Museum of Natural history has my thanks for her continuing accommodation of Pitt anthropology students in allowing me to examine great ape skeletal specimens to reaffirm certain aspects of my comparative analysis.

My colleagues at the University of Pittsburgh provided a great deal of support in all phases of this dissertation. In particular, I thank Dr. David P. Stump for our frequent discussions and his unique insight into problems of systematics and science in general. My friend Robert O'Gwynn provided a great deal of support in the management of image, publishing, and presentation software.

The support of my mother, who never doubted that I would finish, and my father, who did not live to see its completion, was critical to the successful completion of this project.

Finally, this dissertation would not have been possible without the continued love and support of my wife, Angela Kaye Lockard Reed. Angela, thanks for holding down the fort. And Ella, thanks for making it all worthwhile.

James Christopher Reed
April, 2006

1.0 THESIS AND RESEARCH ORIENTATION

1.1 INTRODUCTION

One of the great attributes of Anthropology as a discipline is that it has borrowed freely from and used techniques developed in other disciplines, such as radiocarbon dating in archaeology. Not to say that Anthropology and its subdisciplines (usually divided into four – sociocultural, archaeology, linguistics, and physical anthropology) are not grounded in their own epistemology. Another example of this adoption of another's program can be found in human osteology, where there has long been an interest in how much information – both cultural and biological – can be gleaned from human skeletal material recovered in an archaeological context. For an anthropologist, a human skeleton has a wealth of information about individuals and past populations, from health, diet, and disease to activity, violence, and demographics. Why do anthropologists examine human skeletal material? There are two kinds of general lines of investigation that demonstrate how and why anthropologists take many, many measurements or record the most minute differences in skeletal morphology – forensic anthropology and bioarchaeology/osteoarchaeology. Both ask very similar questions, and both use very similar or the same techniques when analyzing skeletal material. The key is generally to build a profile of an individual or group. Who was the individual? What is the age, sex, height, etc. of the individual? To what group did they belong?

Forensic anthropology asks these questions in a modern medico-legal context, whereas osteoarchaeology goes beyond the “stats” of a single individual skeleton and focuses on the persona of the individual in the group, whether it is historic or prehistoric.

To these ends, many osteologists turn to various standards of measurements or nonmetric traits to answer questions about migration, marital patterns, status, and paleodemography. The tradition of analyzing these traits in physical anthropology has been borrowed from one specific branch of biological systematics – numerical taxonomy, which is often called phenetics. As pheneticists seek to reconstruct evolutionary relationships using overall similarity, physical anthropologists have compared the similarity of human groups to determine their relatedness. This means, however, that the analysis of human skeletal morphological traits fails at the same logical points as phenetics. Currently, there is little acknowledgement of just how much numerical taxonomy has influenced biological distance study in physical anthropology or of the problems inherent in the current methods.

While the excavation and analysis of human burials, either in an archaeological or forensic context, have been primary foci for anthropologists; in the late 1970’s they garnered even more attention. With the coining of the moniker “bioarchaeology” (Buikstra, 1977), a new subdiscipline within physical anthropology was born. Not that bioarchaeology encompassed any genuinely new ideas at the time, but its formalization did create a new focus on the systematic study of human burials coupled with the study of human remains, as is demonstrated by all of the literature on the subject that was subsequently published (e.g. Boddington et al., 1987; Chapman et al., 1981; O'Shea, 1984).

The basics of human osteological analysis have been synthesized into a single volume that has become known as the “Chicago Standards” and is the culmination of decades of technique development and accumulation of experience by many osteologists (Buikstra and Ubelaker, 1994). Included in the volume are instructions on what data to collect, how to collect it, and pre-printed forms to catalogue and measure every trait. The standard interpretation that follows the measuring and recording of traits is usually a statistical analysis of the significance of the frequency of presence of a given trait or set of traits. Both of these steps in skeletal analysis have fundamental problems. First, the lists of traits presented in the book of standards, or from any publication on the best traits or measurements to use (e.g. Donlon, 2000; Pardoe, 1991), constrains or eliminates the important heuristic stage of investigation. Most of the measurements and traits listed and used in osteological studies have been in these lists for decades and are the result of habit and tradition, with little consideration of the nature of the traits or of their use in a given study. For instance, although anthropometry had been around since the early days of physical anthropology, it was not until the latter part of the 20th century that any test was done on the possible heritability of metric traits (Sjøvold, 1984). All of the traits typically recorded by the osteologist are found throughout all human populations, and the assumed genetics responsible for the phenotype varies in the same manner. The broad collection of scores of the variation of these traits, specifically in terms of their frequency, is used to delineate populations.

But does a test of statistical significance of trait differences between already-defined populations define these groups biologically? If these populations, as culturally

defined, are assumed to have a biological "signature," would an analysis of frequency of traits be the best way to delineate groups?

If we look at why we use statistics, the answer lies in the questions we want to answer about these skeletal traits. Statistics is used to estimate and to make predictions of outcomes given specific types of data. But what are osteologists predicting when they make these calculations? What are they estimating? If the particular research program is about the relationship between stature and health, and we want to estimate stature given certain health conditions, such as nutrition, then that's a reasonable use for the statistical analysis of cumulative data. But to use the frequencies of nonmetric traits or the central tendency of a particular cranial measurement as traits themselves is to *describe* the nature of the population, not to *define* it. When osteologists start with a cultural, linguistic, or geographical limit on the population sample to be analyzed, the group has been defined beforehand, without regard for the possible biological relationships of the individuals in the sample, if there is indeed one. To compare trait frequencies to see which groups share a similar pattern of frequency of trait expression in order to argue that these groups are more similar than another, is to use of numerical taxonomy, or phenetics, to suggest biological relationships through the amount of similarity among various groups.

1.2 THEORETICAL ORIENTATION

Differences in human groups should be viewed as representative of historical events; evidence of a historical point of genetic and phenotypic change. As a hypothetico-

deductive approach, cladistics is the preferred method for reconstructing these historical events. Anthropologists have stated that they are not reconstructing phylogeny. Perhaps anthropologists are not reconstructing phylogenies in the strictest sense of revealing species or higher-level monophyletic groups, but the assumed mechanisms of change – mutation, natural selection, developmental change, etc. – are the same, regardless of a hesitation to see the art of delineating potentially different human groups as part of a phylogenetic analysis based on hypothetico-deduction, the stated purpose of cladistic analysis is to reconstruct historical events, the branching hierarchy of phylogeny, thus making it the appropriate methodological and theoretical foundation for biodistance analysis. Specifically, the "sophisticated falsification" – testing alternative hypotheses with a high amount of empirical content resulting in an accumulation of corroboration – suggested by Kluge (1999) should be used as the theoretical foundation for determining the possible biological affinities of human individuals and groups.

In contrast to other approaches, including phenetic analysis, cladistic embrace the fewest assumptions possible. From the outset, physical anthropologists make assumptions that specifically concern the identification of the group under analysis. For example, even though skeletal samples generally do not represent breeding populations, anthropologists often make that very assumption to simplify their analyses (Saunders, 1989). The analysis of matrilocal residence patterns, historically a major focus of biodistance analysis (Larsen, 1997), also demonstrates the use of problematic assumptions. In order to use traditional biodistance methods to determine residence patterns, the groups are first defined the varying morphology of individuals is then compared. This type of analysis assumes the groups that have been previously

defined, generally by cultural means, are also, somehow, morphologically distinct enough to be compared to other groups. But it is this very distinctness of morphology that should be tested prior to any other type of analysis. Ideally, morphological comparisons should be based on the biology of individuals and not on cultural or linguistic boundaries.

1.3 HYPOTHESES FOR THIS PROJECT

Theoretically, groups that share the most unique, derived characters are the most closely related. This hypothesis, however, must then be tested against alternatives. Each test that fails to refute the favored hypothesis strengthens that particular hypothesis by virtue of corroboration (Engelmann and Wiley, 1977). The characters to be used in such an approach to biodistance need to be unique, or at least present in a unique form of an already known trait.

How does one isolate characters to be used in a cladistics-based analysis? In a typical biodistance analysis, the choices of traits to use is pat; lists are standard (Buikstra and Ubelaker, 1994). These lists are conducive to phenetic/probability analysis, because they focus on traits that are found in every population. But for a cladistic analysis to be applied to human skeletal samples, unique traits, or alternatively, unique forms of already known traits must be illuminated in the appropriate samples. As such, traditional trait lists fail to be informative for delineating related groups or individuals.

The primary hypothesis for this investigation is: given a known sample of related individuals, unique nonmetric characters can be delineated demonstrating the biological distinctiveness of that group. In testing this hypothesis, two secondary research questions will also be considered:

- At what level can unique characters be found? Only at the sample level or only in higher levels of a hierarchy.
- How well-preserved do the specimens in a sample need to be? Can partial skeletal elements be used? Or must the whole bone, for a many of the many of the individuals, be in reasonably good condition for adequate comparison?

1.4 CHAPTER SYNOPSES

Chapter 1 summarizes the basic problem to be assessed in this project, as well as the approach for conducting the research. Included in this chapter are an overview of the specific problems in biodistance addressed in the early chapters of this thesis, an overview of the theoretical orientation, and the hypotheses that underlie this project.

Chapter 2 is an overview of the history and traditional methods of skeletal analysis used in physical anthropology. The chapter focuses on how osteologists have historically viewed morphological differences between humans, including concepts of racial differences in general world populations as well as populations specific to a given continent, such as North America. Osteologists have long associated the frequent appearance of specific morphological characters with perceived racial differences.

Specifically discussed are the history of the view of different human groups, which for much of the history simply focused on racial typology, and why these views are now no longer considered valid. Also discussed are current accepted methods of skeletal analysis, especially those used to determine if individual remains "belong" to a specific population or subgroup, such as with the determination of race, or ancestry, in forensic cases.

The final portion of this chapter outlines the modern history of the analysis of nonmetric skeletal traits, specifically the theories of the genetics behind their appearance and how they have been and are currently used to determine the probability that individuals belong to the same group.

Chapter 3 discusses biodistance – the analysis of biological distances of population samples – how specific concepts of genetics, such as epigenetics, developmental genetics, and mitochondrial DNA, affect the approaches. This chapter discusses in detail the different views of the affects genetics and epigenetics have on the appearance of skeletal traits. Also discussed is how animal models, specifically Grüneberg's mouse models, have been applied to nonmetric characters of the human skeleton.

This chapter also describes current methods for evaluating possible biological relationships between population samples. These current and widely used methods of determining biodistance are grounded in phenetics. This review also includes an examination of how phenetics has directly affected biodistance analysis, and thus how biodistance methods carry the same problematic baggage that plagues phenetics.

Chapter 4 evaluates cladistics as the most appropriate method for the reconstruction of historic events. The discussion focuses on the specific logic behind cladistics, which is a hypothetico-deductive approach to phylogenetic reconstruction. Events that have affected the course of evolution are regarded as historical in nature. The usual means of estimating phylogenetic relationships through the average appearance of similar characters in extinct and extant organisms is not a valid approach, according to the tenants of cladistics. Since a historical event is a singular event, it can only be a hypothesis which, in turn can only be tested hypothetico-deductively.

Also discussed in this chapter are the traditional characters used in biodistance analyses and why these traits are chosen for analysis. How the frequency of their appearance in a given sample is used to calculate a frequency to be compared to other samples is critiqued as well. Finally, the hypotheses for the entire project are stated in order to clearly direct the research in examining biodistance methods.

Chapter 5 presents the research methods of the project. The methods are straightforward and directly address the issue of the uniqueness of nonmetric skeletal characters and whether samples and populations can be delineated. If the latter is possible, the biological distance between populations could then be determined. Also included in this chapter are the overviews of the samples on which data were, and the significance of the samples for this project, which were selected because they are historically documented and in almost perfect condition (the Spitalfields sample), a

broad interpopulation sample that is well preserved (the Terry collection Sample), in archaeologically excavated and in relatively good condition (the Campbell's Farm and Perry Site samples). The various samples are of historical individuals of known relationship, individuals that have no known relationship, and archaeological samples that are typical of what most osteologists use in their research.

Chapter 6 is an overview of the data and analytical results of this project. The choice and scoring of each character is explained. Skeletal features were documented photographically, and photographic examples are given in this chapter.

In light of the results of this investigation, *Chapter 7* discusses the problems inherent in pursuing biodistance analysis, beyond those of a phenetics-based approach. This chapter also gives the conclusions of the study, whether or not biodistance is a viable course of research given the philosophical problems presented by phenetics and the usefulness of cladistics at this level of analysis. The focus of the project is the usefulness of morphological traits of human skeletal material in biodistance analysis, and the final evaluation of this usefulness is given in this last chapter.

2.0 PHYSICAL ANTHROPOLOGY, TYPOLOGICAL ANALYSIS, AND BIODISTANCE ANALYSIS

2.1 INTRODUCTION

One of the main subjects of research for physical anthropologists is the study of biological differences between people from around the world. Regardless of how scientists question differences between and among groups of people today, physical anthropology has its beginnings in the naturalists of the Enlightenment's focus on classification. There are two parts to the history of grouping people according to their described biological characters. The first is the legacy of racial typology. The second is the concept that human differences are simply of the physical variations of a particular species, *Homo sapiens*. The former idea was used to create arguments of the superiority of one group of people over another (Brace, 1982). The latter concept is that phenotypic variability represents the differential expression of gene frequencies that reflect adaptations to different environments (Buikstra and Ubelaker, 1994).

The physical differences apparent in different groups of people are often attributed by physical anthropologists to accidents of ancestry because distinct physical traits are supposed to reflect genetic isolation at some point in a group's history. Physical anthropologists have used such markers to solve problems such as attributing possible ancestry to unknown individuals in forensic cases and migratory patterns in the

peopling of the New World. The logic of these analyses is that groups will tend to have certain values of measurements of the cranium or specific skeletal variants, and those that share such traits will be more closely related than others. The justification for using these types of data comes from the rise of neo-Darwinian ideas in evolutionary theory in the 20th century, specifically in the fields of population genetics and numerical taxonomy. This theoretical foundation has given physical anthropologists and skeletal biologists tools to demonstrate the genetic distance and biological relationships – or biodistance – between various groups of humans found throughout the world (Pietrusewsky, 2000).

As with any scholarly endeavor, the history and development of "biodistance" analysis is burdened with assumptions and the idiosyncrasies of intellectual legacy. Because anthropologists often borrow unfamiliar techniques and theory from other disciplines, a summary and evaluation of biodistance analysis is warranted.

2.2 RACE, TYPOLOGY AND EARLY PHYSICAL ANTHROPOLOGY

While physical anthropologists now believe that the concept of race as it was originally conceived is no longer a useful or legitimate idea, its affect is evident in how questions are framed within physical anthropology. Skeletal biologists/osteologists often find themselves confronted with the question of biological group affinity for an individual skeletal specimen or group of specimens. How did this particular question become important to physical anthropologists?

The beginning of physical anthropology is almost coincident with that of racial classification through the articulation of descriptive anatomical characters of humans by natural scientists trained in the traditions of the Enlightenment (Armelagos et al., 1982). Many natural scientists of the time believed not that organisms evolved, but that that they appeared in multiple events. This concept is called polygenesis, and was extended to the different races of humans, and that each appeared separately (Bowler, 1989). It was assumed that different groups were significantly biologically different because of their appearance, and thus European anatomists and biologists established metric criteria to create data sets in order to evaluate the differences in the various ”races” (Saunders, 1978). In one of the early attempts at racial typology, Pieter Camper, a Dutch human anatomist, measured the angle of the projection of the face of different groups of people and nonhuman primates (Armelagos et al., 1982; Bowler, 1989). He determined that Europeans fit a Classical ideal, and that Africans had facial angles that fell somewhere between the European ideal and the apes. Camper did not agree with the premises of polygenesis, and did warn against seeing possible similarities between apes and any group of humans as having any significance (Bowler, 1989). In spite of this, Camper’s ideas were assumed by polygenists to argue that the different races are separate species (Schwartz, 1999c).

Johann Friedrich Blumenbach, the father of physical anthropology, also thought there were significant differences between groups of humans. In his classification of different races of humans, Blumenbach (1795) relied on his collection of human crania and used biometric analysis to delineate different human groups (Armelagos et al., 1982; Buikstra and Ubelaker, 1994). Blumenbach agreed with other natural scientists,

such as Maupertuis and Buffon, in thinking that Europeans represented the “original” form of human, and that other races had somehow degenerated because of exposure to unsuitable ecological conditions in other parts of the world (Bowler, 1989). As such, the perceived resemblance of particular groups of humans to apes did not have any evolutionary significance. Blumenbach, perhaps more forward-thinking than other scientists of his day, also criticized the use of the facial angle in arguing that different groups of humans were created through polygenesis. For Blumenbach, the important aspects of the human anatomy are not those that could be superficially compared to that of an ape’s, but the characteristics that are common to all humans which set them apart from all other animals. This has, in large part, contributed to phylogenetic thinking (Schwartz, 1999c).

The idea that some human groups were more primitive than others was entrenched long before evolutionary ideas began to flourish, but, ironically, it was the acceptance of evolution by natural scientists that led them to try and organize a “scientific” basis for a hierarchy of races. With Haeckel’s Biogenetic Law, evolutionists who argued that a hierarchy of the races of humans existed had a seemingly reasonable theory for support (Saunders, 1989). Haeckel stated that the embryo of an organism, during its development, passes through different adult stages that represent different forms of life. Development is arranged from the lowest form in early development to the end form, representing the highest level for that organism (Haeckel, 1896). Some scientists, in keeping with Victorian European ideals, believed that the highest level in nature is the human and the humans at the top of the Great Chain of Being were the Europeans. Natural scientists who advocated some sort of racial

hierarchy were able to use Haeckel's concept to state simply that at the end of the development of the human fetus, the final stages the individual passes through are those of the different races, from the perceived lowest to the highest. With Europeans at the top of this hierarchical scheme, groups thought to be more primitive, such as Africans, theoretically had more physical characters associated with other animals than did white Europeans (Saunders, 1978).

This is the legacy of early physical anthropology. Indeed, Brace (1982) argues that physical anthropologists have inherited two general spheres of study – paleoanthropology and human variation which the latter has historically been the study of race. Although there may have been little of the idea of the perceived superiority of a particular group by physical anthropologists, groups of people were often considered to be from particular "stocks" (e.g. Neumann, 1952). The general idea was that isolated breeding populations, whether African, European, Asian, or Native American could be delineated by physical characters.

Early American physical anthropologists were trained in Europe with an emphasis on a historical and descriptive approach that was based on the idea that human groups are both biologically distinctive and relatively isolated entities. Pre-Darwinian notions of the biological discreteness of different human groups guided the mostly descriptive work of anthropologists which stressed the differences in skeletal anatomy. Any similarities between groups was thus explained as the result of gene flow between populations (Armelagos et al., 1982).

Samuel George Morton, a Philadelphia doctor and perhaps genuinely the founder of physical anthropology in the United States, conducted the first real

systematic comparison of Native American crania in an attempt to delineate different groups (Morton, 1839). Morton's work had little impact in North America, except in its unfortunate use in defending slavery. In Europe, where the social issues of the U.S. were relatively remote, Morton's ideas had a great deal of influence, especially on Paul Broca (Brace, 1982). Broca, who is most well-known for his pioneering work in human neuroscience, founded the Société d'Anthropologie in Paris in 1859, the express purpose of which was to promote the concept of polygenism (Brace, 1982). Broca elaborated upon Morton's ideas in anthropometry (Broca, 1875), and the theories and practices of anthropometry were widely adopted on the European continent and in England (Brace, 1982). In turn, the important figures of early modern American physical anthropology, who were educated in Europe, brought what were essentially Morton's expanded ideas back to the U.S. and continued the tradition of typological thinking (Brace, 1982).

The two figures who planted the seeds for modern physical anthropology in the U.S. were Earnest Albert Hooten and Aleš Hrdlička, who perpetuated and also changed the view of racial typology (Brace, 1982; Stewart, 1979). The research and methods of Hooten influenced physical anthropology from the 1920's through the 1940's. Hooten focused on using racial typology to reconstruct the biological history of a particular group (Armelagos et al., 1982). He and his students have been associated with the persistence of what Brace (1982) has called "the romantic conception of race." Hooten completed his academic training in Great Britain, and the romantic ideas of race and biology that come from the Scottish Enlightenment and the Age of Reason greatly influenced his training. It is because of Hooten and his intellectual progeny, such as

Carleton Coon and Georg Neumann, that ideas of discrete populations of races were perpetuated in American physical anthropology (Armelagos et al., 1982; Brace, 1982; Schindler, 1985).

Hooten accepted as fact the existence of race, and was perhaps unaware of the romanticizing of racism that pervaded his work. Aleš Hrdlička, on the other hand, was keenly aware of the racist underpinnings of the intellectual framework on which his fledgling discipline was founded. In spite of this awareness, he did enable the use of the same stereotypical ideas, in part because of his idealization of the French school of biological thinking and concepts he took directly from Broca.

Hrdlička is often regarded as the leading influence in modern American physical anthropology. He founded both the leading professional association, the American Association of Physical Anthropologists, as well as the leading professional journal, the *American Journal of Physical Anthropology*. It is difficult to overstate the influence Hrdlička had on physical anthropology. Hrdlička's work, while not evolutionarily based, was grounded in a view that the function of one's anatomy is reflected in its morphology. He also condemned the racism inherent in Broca's anthropology. Even though Hrdlička did not view racial principles as valid, and in spite of the largess of his professional legacy, racial typology persisted in physical anthropology (Brace, 1982).

The idea that groups of people can be delineated through a few measurements or anatomical variants persisted through the middle of the 20th century, with much of the focus falling into two realms of study – archaeology and forensic anthropology. For example, with Carlton Coon's work in the 1930's about different racial groups of Europe, the romantic idea of race as a valid concept was certain of its continuation (Brace,

1982). Coon was probably the most direct intellectual progeny of Hooten. For Coon, races were separate species that arose from parallel evolution (Brace, 1982; Coon, 1963; Weiss and Chakraborty, 1982).

2.2.1 Race and Forensic Anthropology

One current and prominent example of the continuation of racial concepts is the practical application of race in the realm of forensic science. Forensic anthropologists accept that there are measurable differences between the major racial groups to be found in North America; this is one of the cornerstones of forensic anthropology. The possibility of determining differences between subgroups of major populations, or different groups of American Indians or Europeans, for instance, also continues to be a point of research and discussion (St. Hoyme and İşcan, 1989). The use of specific measures of the human cranium have been, and in many cases continue to be, used to build individual profiles in order to help resolve criminal investigations that involve human skeletal remains. The concept is very much the same as when osteologists examine archaeological skeletal samples – the group is defined first and then measured and analyzed for differences. In the early days of forensic anthropology, for modern North American populations, practical classifications meant looking at essentially two groups – white and black. Later studies also purported to delineate characteristics of Asian (often unfortunately called Mongoloid) and Hispanic groups (Stewart, 1979). Different levels of government often require individuals to declare their affiliation with a particular group – White, Black, Hispanic, etc. – for items such as driver's licenses and census-taking. The use of race in forensic anthropology is, therefore, bureaucratic –

governments at all levels insist on classifying their citizens according to race. Forensics, by definition, is concerned with legal matters, and forensic anthropologists are obliged to make a determination of race when possible (St. Hoyme and İşcan, 1989). Forensic anthropologists argue that delineating racial groups is not about defining race or pigeonholing people into groups, but about making a determination about which socioethnic group a particular individual associated in life. In the end, forensic anthropologists simply want to do everything they can to solve an investigation using all of the possible evidence available to them, including the likely ancestry of an individual.

2.2.2 Prehistoric groups

Other than in forensic contexts, most of the focus in physical anthropology has been on describing the skeletal characters of the remains of individuals of different groups found in a prehistoric, archaeological context. Georg Neumann continued the application of racial typology in the analysis of human skeletal remains of prehistoric Native Americans (Neumann, 1952). Neumann's specific research interest was how the New World was originally peopled. To emphasize his assumption that the New World was originally populated by people who migrated from Asia, he classified American Indians in a group – really a subspecies of human in his view – he labeled Mongoloid (Armelagos et al., 1982). He associated different cranial types with different locations, tribes, and general language groups, such as Iswanid, Siouan, or Algonquian (Neumann, 1952; Reed, 1998; Schindler, 1985). The classification of archaeological

populations by associating them with indigenous peoples has continued into relatively recent research (e.g. Kwachka, 1994; Phelps, 1983; Sokal, 1988).

Neumann had a specific analytical procedure to determine the cultural affiliation of the remains of North American Indians, which consisted of four steps. His first step was to measure as many crania from as many different areas and strata as he could. Secondly, he reduced the number of data points by calculating the distributions of their means and standard deviations, and then examined the variability of the data and determined which characters appeared to be diagnostic of a particular group or groups. Third, Neumann eliminated group samples that were too small to possibly be representative of a larger population. Fourth, he compared analytical data between different samples to determine correlations between the physical characteristic of crania and traditional cultural and linguistic groups (Neumann, 1952).

The analytical approach presented above is well-known to anyone familiar with the archaeological analysis of human skeletal material. The significance of the explicit method discussed by Neumann is that it represents a shift in basic thinking about the definitions of different groups. Neumann's starting point was the *archaeologically defined* culture. He then turned to cranial characters already associated with a particular archaeological assemblage. The explicit steps of his method for analysis and determination of the affiliation of crania with groups are an important window into the early part of the developing field of biological distance analysis. But it was Neumann's expectation of the archaeological data to define the cultural assemblage, which presumably defined the breeding group, that bridged traditional racial typology with the analysis of archaeologically recovered remains that influenced later research (Schindler,

1985). While racial typology is a part of the history of human skeletal analysis and physical anthropology in general, its affect on recent research is debated. Some researchers do not think that racial typologies, specifically Neumann's ideas, have affected research in physical anthropology in more recent years (Szathmary, 1985).

Other authors suggest that Neumann's morphological analysis of groups did have a lasting effect on North American osteoarchaeology (Armelagos et al., 1982; Reed, 1998), even if it is not currently validated by osteologists (Ubelaker, 1989). Nevertheless, it is true that the way in which physical anthropologists view groups of people has been influenced by racial typology. While in this era of genetics the old-fashioned views of early anthropologists seem even more out of date, the legacy of racial typology can still affect how anthropologists frame their work. Forensic anthropologists who must deal with race as a legal matter are directly affected by racial typology. Archaeologists are somewhat removed from what Brace (1982:24) calls the "embarrassment of the specific traditions" of racial typology in physical anthropology due to the remoteness in time of their subjects, but they are still using a typological model. Continued use of a "historical-descriptive model" of categorizing human groups has proven to be a major barrier to the development and application of new methods and theories (Armelagos et al., 1982). Several alternatives have been proposed, notably models of adaptation and functional morphology (Armelagos et al., 1982), and the frequencies of specific genetic markers (Brace, 1982; Weiss and Chakraborty, 1982). Even with these alternative approaches to studying differences between human groups, the assessment of basic cranial morphology and measurements is the mainstay of skeletal analysis. Current analysis of different archaeological delineated human

groups focuses on examining the frequency of traits present, or the differences in specific measurements of the crania.

2.3 TRADITIONAL ANALYSIS OF NONMETRIC SKELETAL TRAITS

The methods of delineating groups in either a medicolegal or archaeological context are very much the same. Anthropometrics and discrete anatomical characters are both used to determine the possible biological affiliation of individuals and groups. Most of the early forensic work on race group determination was based on craniometric analysis (Giles and Elliot, 1962), as were most of the initial studies in biodistance (Howells, 1951; Pearson, 1924; Pearson and Woo, 1935). Indeed, a great deal of energy was expended in the early part of the 20th century to develop and standardize measurements and indices that would bear out the biological relationships of different human groups (Armelagos et al., 1982). Metric analysis is still a mainstay of any basic skeletal analysis, whereby specific measures are plugged into formulae to determine if a specific cranium or set of crania belong to a specific group (Howells, 1995; Pietrusewsky, 2000; Relethford, 1994). Some of the measures used have changed very little over the last century. While Camper's facial angle has long since been discredited, many cranial measures that were used a century ago are still in use to today. For instance, the cephalic index is still often used to demonstrate differences and similarities in crania, even though Franz Boas long ago suggested that the index was inappropriate for the determination of the racial affiliation of an individual (Armelagos et al., 1982). The most common measures employed today can be found in

basic texts on human osteology (Bass, 1987; Buikstra and Ubelaker, 1994; Schwartz, 1995).

The other class of characters used to describe the anatomy of the human skeleton is discrete anatomical variants, often simply called nonmetric traits. Nonmetric traits have been touted as perhaps more useful than metric analysis for two reasons. First, metric analysis has been closely linked to racial typology, even though there is an assumed genetic component. The argument has been made by some researchers that nonmetric traits may be more closely linked to genetic control than metric characteristics, and may demonstrate a more likely scenario of genetic relatedness (Armelagos et al., 1982). Second, for metric traits to be of much value the entire skeletal element to be measured, usually the cranium, must be fairly well preserved for there to be any possibility of finding significance in the analysis. The entire skeletal element is not necessary for the analysis of nonmetric traits, only the parts that contain the traits to be analyzed. This is particularly valuable for those who study archaeological remains, which are rarely complete (Saunders, 1989; Tyrrell, 2000).

2.3.1 Animal models and the application of nonmetric trait analysis

The classic studies in nonmetric variation of skeletal material began with the experiments on the heritability of morphological skeletal traits in mice conducted by Grüneberg from the 1940's to the 1960's (Grüneberg, 1943; Grüneberg, 1950a; Grüneberg, 1950b; Grüneberg, 1952; Grüneberg, 1963). Grüneberg crossed "pure-strain" mice, i.e. those that were consistently expressed nonmetric traits, and crossed them with hybrid strains (Grüneberg, 1952). He demonstrated that there is not a simple

relationship between genetics and morphology (Grüneberg, 1952; Saunders, 1978), that genes alone do not control the form of traits. The phenotypic expression of nonmetric traits can also be affected by the epigenetic events of development (Berry and Berry, 1967; Saunders, 1989). Morphological traits were subsequently dubbed "quasi-continuous" to denote the control of multiple genes and the influence of the environment on traits, and to demonstrate a genetic remoteness from the phenotype (Grüneberg, 1952).

The theory and method of Grüneberg's studies of nonmetric skeletal variation in mice were co-opted for studies on human skeletal nonmetric variation. Berry and Berry with coworkers (Berry and Berry, 1967; Berry et al., 1967; Berry, 1963; Berry, 1968; Berry and Searle, 1963) applied the methods developed from rodent studies to the analysis of the human skeleton and stated that nonmetric trait frequencies can be used as genetic markers for variability in human populations (Berry and Berry, 1967; Saunders, 1989). The overall positive tone of the Berry and Berry articles suggests that nonmetric traits are superior to metric traits in biodistance analysis because incomplete skeletal elements could be used, whereas metric analysis generally requires the complete bony element (Saunders, 1989; Tyrrell, 2000).

The analytical program initiated by Berry and Berry assumed a direct correlation between genes and observable skeletal form. This is a departure from Grüneberg's emphasis on quasi-continuous traits (Saunders, 1989). The assumption of a direct relationship between the genotype and phenotype ignores any possibility of effects related to age, sex and size or side of body as well as environmental effects (Saunders, 1989). There is an epigenetic aspect to the phenotype (Berry and Berry, 1967). In

other words, the development of the human skeleton, and any biological system, is affected not only by genetics, but also by environmental factors (Løvtrup, 1974; Waddington, 1960). Osteologists have since emphasized the importance of epigenetic events in the development of phenotype, and the influence of sex, age, size, side and environmental factors on the phenotype (Buikstra, 1972; Corruccini, 1974; Finnegan, 1978; Kellock and Parsons, 1970; Ossenberg, 1970; Saunders, 1978; Saunders, 1989; Tyrrell, 2000). While there is not a simple one-to-one correlation of gene-to-phenotype, osteologists insist that there is value in the analysis of nonmetric traits and their assumed genetic underpinnings (Donlon, 2000; Konigsberg and Buikstra, 1995; Sciulli, 1990; Sempowski and Spence, 1994).

2.3.2 Current standards of analysis

Questions of how genetic instruction controls the formation of the skeleton and other characters of anatomy have led, in some part, to differences in the lists of traits used in biodistance studies (Figure 2.1). But for the most part, the characters that have been used in biodistance analyses have changed through the years because different researchers have placed different emphases on a given set of characters, either because of limitations placed on the analysis by the preservation of the human remains, or changes in the perceptions of the likelihood that the trait will be inherited. Sometimes it seems as though the traits commonly employed in biodistance analysis are based on personal experience – what the researcher intuitively thinks works best. A great deal of the effort in human skeletal analysis generally has been based on a multitude of personal experiences which has served to increase the difficulty of relating and

comparing the data of different studies. Personal differences in analyses demonstrate a lack of consistency in method and data collection, which has in the past plagued osteological research in general. To rectify this lack of consistency, standards for the important aspects of human skeletal analysis were compiled, including basic forms and schematics for recording data in skeletal analysis (Buikstra and Ubelaker, 1994). This book is the *Chicago Standards*, and it has become indispensable to beginning and advanced osteologists alike. The book does not, however, list all of the traits that many osteologists view as important. The long list of nonmetric traits used in the comprehensive studies recently completed by Ishida and Hanihara (Hanihara and Ishida, 2001a; Hanihara and Ishida, 2001b; Hanihara and Ishida, 2001c; Hanihara et al., 2003) demonstrate a more complete set of characters used in biodistance analysis.

Both metric and nonmetric analyses have maintained their prominence in recent research, with little favor for one or the other in specific studies (e.g. Donlon, 2000; Hanihara et al., 2003; Konigsberg and Buikstra, 1995; Pardoe, 1991). Phenotypic traits are controlled by genes, but, according to the hypothesis of nonspecificity, no specific set of traits is controlled by a specific set of genes (Saunders, 1978; Sneath and Sokal, 1973). The relevance of the hypothesis of nonspecificity is that similar classifications for any biological group can be produced from different sets of phenotypic characters, including those of humans. Physical anthropologists have been able to use both metric and nonmetric skeletal data for biodistance analysis because the hypothesis of nonspecificity states that the same conclusion for a given classification can be reached with different data sets (Farris, 1971; Saunders, 1978).

2.3.3 Heritability of nonmetric traits

While opinions differ as to which traits are relevant to biodistance analysis, there is a great deal of agreement that anatomical traits can be used to identify groups of related individuals. This assumption is based on the fact that the phenotype is controlled by the genotype, and the belief that similar genotypes should create similar phenotypes. The choice of which traits to use depends on which traits are reliably inherited. The heritabilities – the reliability that a trait will be passed to the next generation – of human skeletal traits commonly used in distance analysis have been calculated (Sjøvold, 1984; Sjøvold, 1995). Heritability for all traits, however, has not been calculated, and the appearance of many seems to be unpredictable (Hauser and De Stefano, 1989).

In reality, there is a problem with comparing the biological traits of different breeding populations, whether human or nonhuman. It is impossible to study all of the individuals of a given species or even a population. It would be extremely difficult to examine an entire living breeding population, and impossible to examine an extinct one, because the biological and geographic limits of the population cannot be known. Skeletal biologists therefore treat excavated remains as a sample of a population of unknown size. There is, however, the assumption that the excavated sample is genuinely representative of the population as a whole (Ubelaker, 1989). The issue of sampling and the analysis of characters were also issues that were problematic for evolutionary scientists at the beginning of the genetic age. Biological and evolutionary theory had advanced to the point where Mendelian genetics and anatomical analyses were joined in the concepts of population genetics. Because distance studies for human groups are based on population samples and genetics, it stands to reason that

some of the theoretical basis for studies in biological distance comes from the field of population genetics.

2.4 POPULATION GENETICS

Population genetics is the application of the theory Mendelian inheritance to the analysis of the frequencies of traits that can be found in a population. The foundation of population genetics came from the idea of “beanbag” genetics, where each trait is controlled by a single gene, and natural selection acts on each gene. In this framework, natural selection selected for advantageous traits, and against detrimental traits. As a result, the genes that are responsible for the advantageous traits would be found in high frequency in a population, and non-advantageous or detrimental genes would be found less frequently (Bowler, 1989).

R. A. Fisher, Sewell Wright and J. B. S. Haldane, who are also famous for unique and useful speciation concepts, are perhaps the most notable names associated with the development of solutions to the mathematical problems presented by population genetics (Bowler, 1989; Fisher, 1930; Haldane, 1932; Schwartz, 1999c; Wright, 1939). Much of the impetus for early population genetics studies was practical. Population genetics was born of the economic need in agriculture to understand details of breeding in order to breed the desired traits in a given agricultural product. For instance, herders and ranchers have long had a vested interest in predicting how to breed livestock with the most desirable traits. Population genetics gave breeders the tools to manipulate their herds to breed for the appearance of the most desirable characteristics for the

marketplace. A large portion of Wright's work was related directly to this particular problem (Wright, 1923; Wright, 1978).

One of the more well-known examples of how population genetics is used in the study of different characters found in populations is represented by the familiar Hardy-Weinberg equilibrium equation. Characters that can be found in any given breeding population represent alternative states of an allele. The equation represents a state of equilibrium – when the alternative states of the character are found in a proportion that is outside of the equilibrium predicted by the equation, the interpretation is that natural selection is acting on that particular trait and selecting for a specific form of the trait. While this may be a simplification of the specific arguments in natural selection, the basic idea is that gene frequencies are represented by the frequency of appearance of phenotypic traits and represent selection for those traits. Therefore it is argued that the differences we see in different human groups are the result of selection acting on these specific traits in a microevolutionary fashion (Powell and Neves, 1999) . In an extension of the argument, the frequencies of traits found in a population of humans, or any group of organisms for that matter, reflects the particular selection pressures on that population.

Evolution is seen by many biologists as a statistical force (Sokal and Rohlf, 1969). Differences in human populations are assumed to be the result of selective and evolutionary forces within our species. If evolution is a statistical force that can be seen in shifts in allele frequencies and the same can be said for changes in human populations, then it stands to reason that differences between human populations can also be determined through statistical analysis.

Population genetics was initially adopted by physical anthropologists to support the use of morphological analysis in the classification of different human groups (Schindler, 1985). While population biology and genetics did influence physical anthropologists in studies of human populations, it did not influence their approach to the subject; they just added genetic concepts to their established classifications of different human groups (Armelagos et al., 1982; Weiss and Chakraborty, 1982). Variation continues to be analyzed within predefined populations. Current biodistance analysis assumes the genetic control of physical traits, and that the calculated difference between individuals or groups is directly correlated with the frequencies of those genes that are responsible for the given phenotype (Larsen, 1997). This calculation of gene frequencies depends on the assumption that different environments and degrees of gene flow will affect the selection of traits in the populations, just as they would in population genetics.

2.5 HUMAN VARIATION, BIOARCHAEOLOGY, AND BIODISTANCE ANALSYIS

By the 1950's, Hooten's influence had waned with the widening acceptance of the evolutionary perspective offered by the Modern Synthesis (Armelagos et al., 1982). Population genetics and Darwinian theory greatly affected how anthropologists viewed human biology. In the studies of the genetic affinities of human groups, physical anthropologists began to incorporate ideas of populations and how differences in the genetics of different group could be measured. The introduction of these new ideas,

however, did not necessarily change the predominance of typological thinking in physical anthropology (Armelagos et al., 1982; Weiss and Chakraborty, 1982).

For skeletal analysis in archaeology, the questions are no longer simply about what a particular group looks like anatomically. Morphological analysis is not the end, but a means to an end. The analysis of the morphology of bone and the attempt to determine group affiliation from the anatomy has moved beyond just finding the bones and describing them to asking relevant archaeological questions about migration, emigration, matrilineal patterns, population boundaries, and social groups (Larsen, 1997). Studies that encompass these subjects and use calculations of biological affinity as their foundation are generally classified as biodistance studies. The shift in focus to asking archaeologically significant questions and not simply stopping at the completed descriptions of skeletal morphology coincided with a shift in overall archaeological theory.

Although it was popular in the 1970's and early 1980's, biodistance analysis fell out of favor in later years (Buikstra et al., 1990). Recently, however, there has been renewed interest, as seen in the work of Ishida, Hanihara, and Dodo being the most recent (Hanihara and Ishida, 2001a; Hanihara and Ishida, 2001b; Hanihara and Ishida, 2001c; Hanihara et al., 2003). These studies represent a comprehensive survey of the world's most complete collections of human remains, and probably the most complete set of studies to date focused on discrete skeletal variants. They are an excellent example of the current methods used for determining biological distance. They also demonstrate the advanced use of statistics and computer modeling to create tree diagrams that show biological affiliation of different human groups.

The conclusions of current biodistance studies are reached from arguments about who is most similar to whom, as indicated by statistical analysis of skeletal traits. The idea that similarity should be used as an indicator for biological distance comes from the next logical step of physical anthropologists' use of population genetics and statistics – the concept of phenetic analysis.

3.0 BIODISTANCE, GENETICS, AND PHENETICS

3.1 INTRODUCTION

As anthropologists borrow theory and method from other sciences, they do so with the intent of solidifying the discipline of anthropology as a genuinely scientific, not simply descriptive, field. An example is the use of radiocarbon dating in archaeology, which is a direct application of a technique developed by physicists to solidly answer questions about date and age in archaeology. Physical anthropologists have chosen to use phenetic taxonomic methods for much the same reason. Phenetics – also called numerical taxonomy (Forey, 1982; Funk, 2001) – was developed as a means of making paleontology and systematics more scientific and less descriptive (Hull, 1985). The statistical analyses used in human biodistance studies have a direct relationship to the phenetic analytical methods used by paleontologists. For those who use phenetics as the guiding theory of their research, their general view is reflected in a statement by Sokal and Rohlf (1969:2), “Biological phenomena can only be discussed in a probabilistic framework.”

Because differences between and within human groups are the result of biological phenomena, it follows that skeletal biologists interested in biodistance would use statistics and methods derived from phenetic epistemology to conduct their research. Phenetics, may not, however, be the best means of reconstructing the

phylogenies of extant or extinct taxa, or for determining the biological relationships between different human groups. For instance, critical discoveries about the genetics of the development of the phenotype have highlighted the problems with the basic assumptions of phenetic analysis. Another approach derived from systematics, one based on cladistic methods of phylogenetic reconstruction, can be used to circumvent the logical problems presented by the assumptions fundamental to a phenetic analysis.

3.2 CONCEPTS OF GENETICS AND THE ANALYSIS OF TRAITS

3.2.1 Thresholds and epigenetics

The general concept of genetics used by anthropologists, which was reviewed briefly in chapter one, presents several problems. Although no one genuinely thinks in terms of a strict Mendelian inheritance, the simple explanation that the phenotype is a mass of polygenic traits is no longer valid. It is true that many genes and gene products (proteins) contribute to the development of the phenotype, but the same genes and gene products contribute to many different aspects of development (Gehring, 1998; Gerhart and Kirschner, 1998).

The overall model of the phenotypic expression of genetic instruction that many osteologists use is a “threshold” of gene expression. It is when genetic expression moves beyond this theoretical threshold that physical expression manifests as an, or suite of, anatomical trait(s) (Grüneberg, 1952; Saunders, 1989). Variation in the expression of nonmetric characters is supposed to be due to a given group’s “liability,” or underlying propensity for the expression of a specific trait according to the threshold

model (Finnegan, 1984; Saunders, 1989). While no one conducting biodistance research really thinks that there is a specific "gene" for a given physical trait, the use of allele frequency as the foundation for determining does seem similar to idea that the threshold is a biological indicator for the delineation of populations.

Thus, the idea that there is a threshold of genetic expression beyond which a physical character is expressed lends itself to continuing the ideas that initially relied on assumptions of alternate allele states. But in this variation on the alternate allelic states idea, individuals either have the proper combination or amount of expression of a gene, or they do not. The degree of expression found in one population versus another is not necessarily a difference in the threshold of expression of a given trait. The variation is thought to be caused by differences in the means of the underlying continuity of the genomes in the populations. In this version of Grüneberg's quasi-continuous model of phenotypic inheritance, the expression of a trait can also be influenced by environmental factors (Saunders, 1989). The idea that the development of physical traits is affected by extragenetic sources has been around for quite some time, but is perhaps best summarized by Soren Løvtrup in his monograph *Epigenetics* (1974). Osteologists have been aware of epigenetic influences, even though defining specific events is difficult if not impossible. One might be aware of the possibility of environmental influences affecting the development of the phenotype, but unable to pinpoint exactly what beyond the genetics is influencing the appearance of certain traits. This sort of assumption is not unreasonable, and is often made in arguments about natural selection and environmental factors in development and survival.

3.2.2 Phylogeny and Developmental genetics

The development of an organism relies not on Medelian inheritance or on a threshold of susceptibility, but on a hierarchical cascade of genetic instruction directing the development of all aspects of the soma, from the initial patterning of the body to the number of follicles in the skin (Gehring, 1998; Gould, 1977; Raff, 1996; Raff and Kaufman, 1983; Schwartz, 1999c). The genes and molecules that control development work in a hierarchical fashion – regulatory genes control genes and molecules downstream in a cascade of information, and there is a subsequent cross talk between the genes themselves (Thorogood, 1997). This communication is the means by which genes regulate and orchestrate the phenotype of an organism. A change in genetic instruction at any level in the hierarchy will result in a change in the form of the organism. The higher up in the cascade of genetic instruction the change occurs (i.e. the more upstream the interference in signaling), the more likely it is a drastic change in form will result. The lower in the hierarchical cascade and later in ontogeny a change in the genetics of development genetics occurs, the smaller the change in phenotype because there is less physical development to affect downstream. Changes in the instruction of ontogeny at any level is now believed to be a force of evolutionary change (Raff, 1996; Shubin et al., 1997). The genetic systems that control the development of the phenotype are much more complicated than a simple linear expression of a set of genes (Weiss, 1993). The comparison of genetic characters for phylogenetic reconstruction should therefore be more than a comparison of sequences, but a comparison of the control systems of development. A reasonable extension of this evolutionary argument is that the physical traits used to delineate human groups are not

the result of basic ideas of inheritance, but of the final part of the cascade of ontogenetic instruction.

The current means of genetic comparison is to compare either nuclear or mitochondrial nucleotide sequences to illuminate similarities between different samples (Stone, 2000). For example, this type of genetic comparison has been used to examine hominoid phylogeny, and to test the phylogenetic hypotheses based on morphological evidence (Collard and Wood, 2000). But even if a phylogeny constructed with genetic evidence is different than that derived from morphological evidence, it does not mean that the phylogenetic hypothesis based on morphological evidence is falsified. For the falsification to take place, one would have to assume that the genetic evidence is intrinsically and immutably correct in its reflection of evolutionary relatedness. Parallelism and the retention of primitive traits, however, can be found at molecular levels just as they as they are in the phenotype. As Schwartz (1988:82) states, "There is no a priori reason why a biomolecularly based phylogeny should necessarily falsify a competing morphologically based theory of relatedness." Molecular data are no more valid as evidence of evolutionary/biological relationships than morphological data (Marks, 1994).

3.2.3 Mitochondrial DNA and the molecular clock

There is an assumption in biodistance analysis that the characters and the "genes" that code for them are evolving at a constant rate across all human groups (Powell and Neves, 1999). This assumption is based on the idea of a molecular clock, where the majority of evolutionary change takes place in sections of the DNA that do not code for

phenotypic expression (Kimura, 1983). Different genes and different parts of genes are supposed to evolve at different rates, and different parts of genes also evolve at different rates (Valentine, 2004). Most analysis does not make use of nuclear DNA, but mitochondrial DNA (mtDNA). mtDNA is purportedly passed to offspring only by the female, and thus theoretically preserves a direct matrilineal link across many generations.

The use of the molecular clock in any biological analysis suffers from the problem that the rate of molecular evolution is not constant or clock-like, especially given the selective pressures on nuclear DNA and the recombination of nuclear DNA (Valentine, 2004). Evidence from the fossil record, specifically the sudden appearance of forms (the Cambrian explosion, for instance,) seems to bear out the conclusion that the molecular clock is not constant (Byles, 1976; Gould and Eldredge, 1977; Tattersall and Schwartz, 2000; Valentine, 2004). The use of mtDNA seems to be ideal for determining phylogenetic or biodistance relationships, given the assumption that mtDNA mutates at a constant, predictable rate because of the lack of selection pressure and recombination. With this assumption one can compare the differences between two organisms, or two individuals, and determine how much time has passed since they shared a common ancestor or relative. In this way, differences and similarities can be measured and a scheme of relationships of taxa or individuals can be fashioned.

Recent research, however, indicates that the assumption of a constant rate of mutation in mtDNA may have been made in error (Hagelberg, 2003; Melnick and Hoelzer, 1993). On one hand, certain parts of the mtDNA strand may be more likely to mutate than others, and, therefore, at a faster rate (Stoneking, 2000). The assumption

of a constant rate of may be erroneous also because of evidence that it may not pass to offspring only from the female, but actually undergoes some amount of recombination during organismal reproduction (Hagelberg et al., 1999; Innan and Nordborg, 2002; Smith and Smith, 2002). There is also evidence from primate genetic research that the phylogenetic data from mtDNA does not parallel data from nuclear DNA in evolutionary analysis. This incongruence means that an evolutionary relationship based on mtDNA would not necessarily reflect the relationships of species or other taxonomic groups (Melnick and Hoelzer, 1993). While not indicating doom for mtDNA studies, "there are enough unexplained patterns in mtDNA to warrant reassessment of the conclusions of many mtDNA studies" (Hagelberg, 2003:89).

The use of DNA in human biodistance is also problematic given the fact that the recovery of DNA from older skeletal material, specifically that which is recovered from the archaeological record, is rare. DNA extraction from skeletal material or from teeth is still an expensive process, as is DNA mapping. Given the prohibitive nature of the expense of using DNA, osteologists must generally rely on the evidence at hand – the morphology of human bone which makes some sense because the phenotype should be considered the primary source of data for comparative study in biology. It is the phenotype on which external (selection) forces act, and which reflects the unique factors that have guided the evolutionarily unique changes intrinsic to a biological group or taxa. In this sense, osteologists must rely on the phenotype to illuminate similarities and differences between human groups, as evolutionary forces – genetic and developmental change internally, and selection externally – are responsible for the differences in human groups. Finally, if human remains are to be studied as part of an

all-inclusive biological hierarchy that includes the fossil record where no DNA is preserved, the same kinds of phenotypic data are best for cross-taxa comparison.

In summary, the genetics of development and the influence of epigenetic events on development suggest that the basic assumptions made by those using phenetic analysis may be too burdensome for a reasonable assessment based on traditional ideas of the inheritance of physical traits.

3.3 BIODISTANCE AND PHENETICS

3.3.1 Phenetics/numerical taxonomy

After the establishment of distance studies in the 1950's and 60's, anthropologists looked to systematists for a way in which to delineate groups of humans on the basis of morphology. In their "populational" studies of the 1960's, physical anthropologists recognized that essentially what was needed was a taxonomy of different groups of human populations. At the time, systematics was in a position to offer different, competing methods and theories to anthropologists – evolutionary systematics, stratophenetics, phenetics, and cladistics (Cracraft, 1974; Forey, 1982).

Physical anthropologists chose phenetics as the appropriate method to apply to the analysis of human skeletal material in order to morphologically and metrically delineate different populations. Phenetics is an approach developed in systematics to group organisms by their overall similarity (Cracraft, 1974; Mayr, 1982; Mayr and Bock, 2002). Specifically, numerical taxonomy is a means by which specific morphological entities could be analyzed, coded, and run through statistical analyses in order to find

the most similar, and therefore the most closely evolutionarily related, forms. The goals of these analyses, as with any study in systematics, are the reconstructions of phylogenies (Sneath and Sokal, 1973; Sokal and Sneath, 1963).

Phenetics was chosen and is still used to analyze the morphology of human skeletal material for the same reason that phenetic analysis was developed in systematics in the late 1950's – to make classification more quantitative, repeatable, and empirical (Hull, 1985). The "average" is an important concept in phenetic analysis, where the mean of the frequency of appearance of a coded trait or measurement is used to show similarities and differences between groups (Wiens, 1999). In a phenetic classification, organisms that belong to a particular taxon are on average more alike than other organisms at a similar taxonomic level (Sokal, 1986). For the comparisons in the analyses, central tendencies of the appearance of characters – essentially the average of any measure in any of the studied populations – are calculated. These central tendencies of characters represent estimates of a taxon, and the compared and grouped characters are estimates of phylogenies based on the frequency of traits found in groups (Wiens, 1999). Statistics are used to estimate and to predict. If the central tendencies of the group can be measured, then there is some level of predictability associated with the analysis. This is not predictability in the sense of foretelling the physical appearance of some undiscovered form, but in terms of the reliability of the outcomes given specific groups (Sokal, 1986). The basic process of using phenetic analysis to reconstruct phylogenies is presented here, following Sokal (1986).

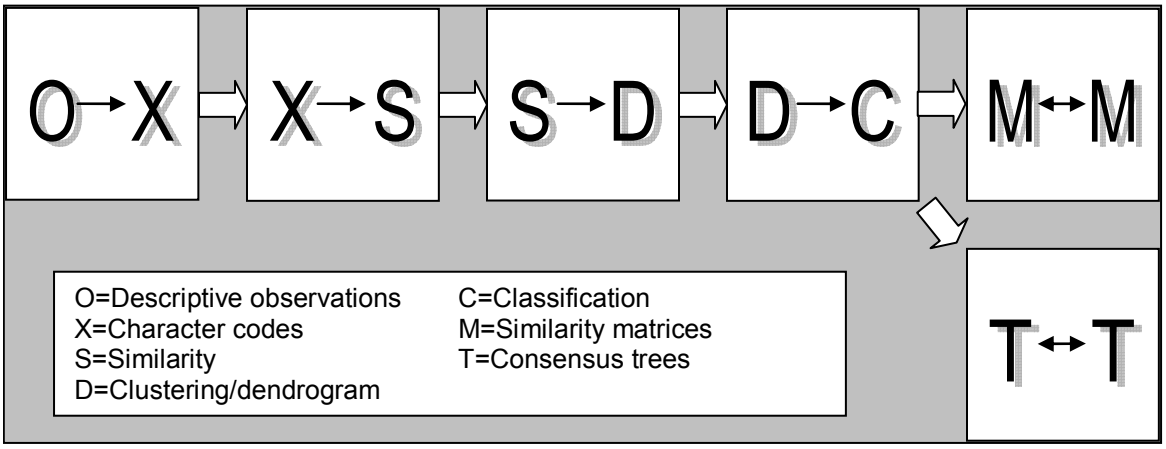


Figure 3.1: Phenetic/numerical taxonomy procedure (after Sokal 1986)

The first phase of any taxonomic analysis (alpha taxonomy) is a description of the specimens and the character states that are to be used in the analysis (Mayr, 1969). After this descriptive phase, the first step in phenetic analysis is to code (represented as O in Figure 3.1) the characters or measurements (represented as X) in a fashion that is conducive to numerical analysis, specifically to facilitate the use of statistical formulae. The codes used for characters are determined by the types of characters used in the analysis, whether continuous, such as a measurement, or discontinuous, such as the presence or absence of discrete anatomical traits.

Once the characters have been appropriately coded, they can then be put through computations that calculate measures of similarity (represented as S in Figure 3.1). Different methods of calculation are appropriate for different types of data. For binary or unaltered multistate data (generally discrete traits), association coefficients are calculated. For measurements and ordered multistate data (generally continuous traits) correlation coefficients are often calculated to test for the greatest amount of similarity.

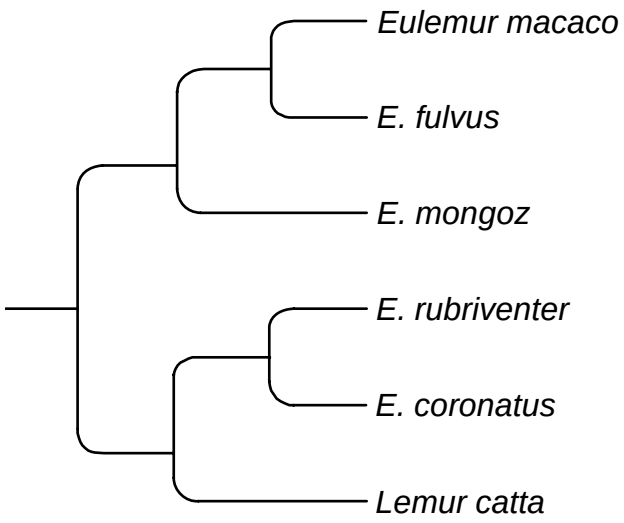


Figure 3.2: Proposed tree diagram of the biological relationships of certain lemurs (after Viguier, 2002)**.**

These quantified similarities are only a numerical representation of a figurative similarity between two groups or individuals. When multiple calculations are completed and then compared through cluster analysis (D → C, Figure 3.1) a complete picture of possible biological relationships can be produced. A dendrogram, which is a graphic representation of the calculated similarity of particular biological groups is then constructed (Figure 3.2). The branches and their relationships that are generated in a cluster (or tree) diagram in representing the phenotypic similarities, also, because of the nature of the genotype/phenotype relationship, represent the genetic similarities of the different groups. The closer the clusters and shorter the branches appear, the closer the morphological relationship, the farther apart, the more distant the morphological relationship, and thus the biological/genetic relationship is revealed. This graphic expression of possible evolutionary relationships is generally the last step in the phenetic reconstructions of phylogenies. Thus, a dendrogram is a graphic representation of calculated similarity, and therefore presumed genetic distance, of particular biological groups (Figure 3.2).

In a phenetic analysis of the relationships of human groups, another step is often employed in the reconstruction of phylogenies. Similarity matrices generated by cluster analyses are compared to illuminate different relationships (S ←→ S, Figure 3.1). Numerical pheneticists argue that these comparisons demonstrate how the taxonomic relationships of groups may be correlated to the historical idiosyncrasies of certain groups, and this can reveal the historical relationships between peoples. Consensus tree methods (C ←→ C, Figure 3.1) are also used for the comparison of results obtained from different types of data, as they have been converted into easily manipulated units.

Specific phenetic/numerical taxonomic methods have been readily applied to biodistance analysis whatever the class of data, because anything can be used as an OTU – operational taxonomic unit – whether, for example it is a measure, an individual, an anatomical character, a geographical location, or an ecological niche (Sneath and Sokal, 1973; Sokal, 1986; Wilmink and Uytterschaut, 1984). In cluster analysis OTU's are transformed into manageable numerical classes and are input into a computational algorithm that generates dendrograms. In phenetic analyses, the unit of measure, or OTU, can be just about anything. They can be actual metrics, data on anatomical traits, or behavior or language in cases of comparative study. The most important detail about these units is that they can be standardized, transformed, and plugged into statistical analyses. The resulting clusters are measures of similarity, clustering those specimens with the most similar measures and the most dissimilar groups having the most distance in the tree diagram (Wilmink and Uytterschaut, 1984). This is often represented in a hierarchical, branching arrangement (Figure 3.2).

Through statistics and cluster analysis, phenetics measures the central tendancy of a trait pattern for group members, therefore "establishing groups based on maximum similarity among [traits] or on maximum predictive value (homogeneity of character states)" (Sokal, 1986:425). For osteologists, the application of statistics to the grouping of individuals by their skeletal traits is directly associated with the multivariate phenetics analysis of Sneath and Sokal and their analysis of OTU's (operational taxonomic units) (Wilmink and Uytterschaut, 1984). The transformations and statistical results allow for widely varying data types to be analyzed and compared.

3.3.2 The statistics of biodistance

Analyses of skeletal traits, whether metric or nonmetric, generally depend on multivariate statistical analysis – mean measure of distance, Malhanobis' distance analysis, or discriminate function analyses (Pardoe, 1991; Pietrusewsky, 2000; Powell and Neves, 1999; Sjøvold, 1973; Sjøvold, 1977). The outcome of these statistical analyses are measures of the variability of traits in and between particular groups within a certain level of statistical significance (Key and Jantz, 1990). In other words, there would be a high degree of probability that members of a particular group have the same variation in the expression of particular skeletal traits. The measure is thus of the central tendency of a particular group to have a certain frequency of the appearance of a trait. Or, as Sokal (1986:425) states:

> …[R]egard these propositions [of classification] as probabilistic, that is, class *A* possesses state *i* of character *j* with a probability of $P_{ij} \leq 1$.

Just as when phenetic analysis is applied in systematics, phenetics in physical anthropology is seeking the *most likely* scenario of relationships between individuals and groups (Powell and Neves, 1999).

The relationship of statistical analysis in physical anthropology to phenetic analysis is not a trivial one. Phenetics is assumed to be the theoretical foundation for biodistance analysis, specifically used as background knowledge for the epistemology of the subfield (Pietrusewsky, 2000). Biodistance uses two lines of physical evidence – continuous, anthropometric data; and discontinuous, discrete anatomical (skeletal) traits. Both are subjected to statistical analyses in order to determine significant differences, if any, that indicate the closeness or the distance of biological relationships of individuals and populations (Donlon, 2000; Pardoe, 1991; Pietrusewsky, 2000; Saunders, 1978; Tyrrell, 2000). This presumed relationship comes directly from the view that evolution, as viewed through the filter of Darwinian theory, should be statistically interpreted. Shifts in allele frequency are often used to demonstrate the action of natural selection within a population. As a result, mathematics has been used in physical anthropology for quite a while. An interest in the determination of past relationships of human groups coincides with the earliest applications of statistical analysis by physical anthropologists (Pietrusewsky, 2000).

There are two basic statistical approaches to the analysis of skeletal traits – univariate and multivariate analyses. Although volumes have been written on the statistical evaluation of the human skeleton (e.g. van Vark and Howells, 1984), several methods commonly employed are (Larsen, 1997): the mean measure of distance (MMD), Mahalanobis' distance, basic Euclidean distance, principle component analysis,

and discriminate function analyses such as canonical analysis (Larsen, 1997; Pardoe, 1991; Pietrusewsky, 2000; Powell and Neves, 1999; Sjøvold, 1973; Sjøvold, 1977).

Univariate analyses are generally used in biodistance analysis to determine if the pattern or frequency of a particular measure is likely to have been caused by random chance. If the frequency of the appearance of a trait or set of traits is determined to be statistically significant, then the frequency or pattern is not due just to random chance, but to some other reason. This other reason, as found in biodistance, is presumably a function of the isolation of a population or some other such force on the distribution of genes and physical traits. The most commonly known statistic of this type is the Student's T test, which gives a result on the significance of a given probability. Univariate statistics, however, are good only for the analysis of specific measurements, and not groups or populations (Howells, 1969; Pietrusewsky, 2000).

The statistical tools employed in biodistance analysis, therefore, are multivariate statistics, which can provide information about the relationships of various characters and the samples from which they come. Saunders (1978) provides an excellent example of the use of the most common statistics in the determination of biodistance using nonmetric traits. The most basic example of a multivariate statistic used is the chi-square statistic. Saunders uses the chi-square to demonstrate associations between the presence of nonmetric postcranial characters and the sex of an individual or the side of the body on which the character appears. Saunders also uses chi-square (with transformations to Yule's Q) to test associations between traits. But for actual group distance studies, Saunders' uses Smith's Mean Measure of Distance (MMD) to determine the similarities of the different samples in her study. MMD was first used by

Berry and Berry (1967) in their seminal article on biodistance (Finnegan, 1984). It has become a commonly used statistic (Donlon, 2000; Pardoe, 1991), but with outcomes having varying degrees of success (Larsen, 1997). Biodistance is , however, expressed in terms of positions and distances in Euclidean space, and MMD does not provide this type of measure (Saunders, 1978). An alternative statistic is Mahalanobis' distance (D^2), which has become a standard for biodistance analysis of nonmetric traits (Larsen, 1997). The results of Mahalanobis' D^2 do provide Euclidean mathematical distances, to the second power (Pietrusewsky, 2000; Powell and Neves, 1999). Another step often taken is the application of a principal component analysis (PCA) which can illuminate what particular variables are the most responsible for the biological distances that have been calculated (Donlon, 2000; Pietrusewsky, 2000; Powell and Neves, 1999)

Whatever multivariate tool is used to calculate distances, cluster analysis is generally the means by which these numerical distances are analyzed and interpreted in terms of groups being either more or less similar to each other. Cluster analyses use algorithms to group individuals by an already estimated variate (Pietrusewsky, 2000). The more overall similarity calculated between the characters of a group, the closer the groups will be clustered on the diagram (e.g. Hanihara et al., 2003; Pietrusewsky, 2000; Wilmink and Uytterschaut, 1984). – just as with the dendrograms (phenograms) of taxa constructed phenetically. The procedures used in biodistance are the same as those used in phenetic analysis, such as UPGMA (unweighted pairgroup method using averages) and Neighbor-Joining (Pietrusewsky, 2000; Saunders, 1978; Sneath and Sokal, 1973).

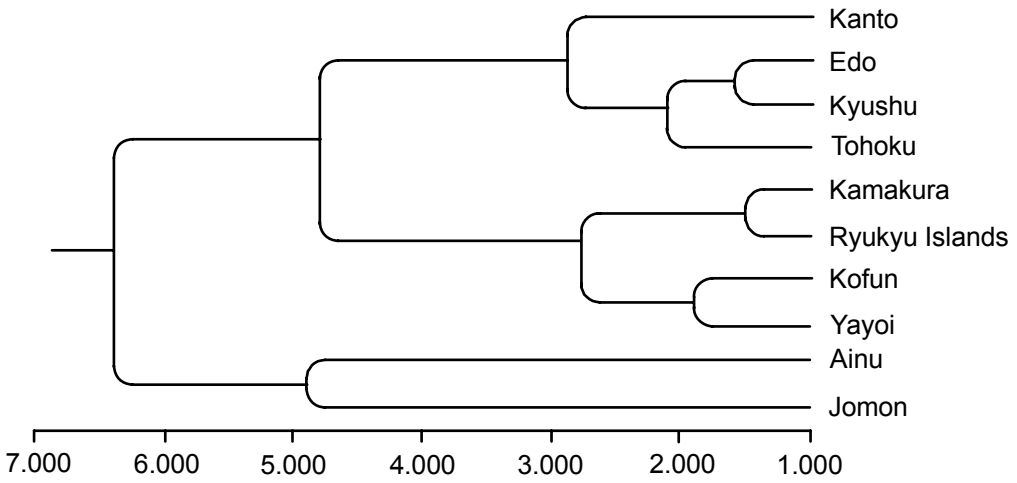


Figure 3.3: Tree diagram of human groups from the Pacific Rim (after Pietrusewsky, 2000).

The ease of use and availability of computers and clustering programs has increased the popularity of cluster analysis. Cluster analysis works by maximizing the effects of the factors/criteria that are shared in the clustered groups, even though clusters are not precisely defined and can shift based on the OTU's used in a given analysis (Wilmink and Uytterschaut, 1984). The clusters are usually presented in a hierarchical fashion to demonstrate that while all specimens may be of the same general group (humans for instance), some groups are more similar to each other than they are to others (Figure 3.3). In their comprehensive study, Hanihara et al. (2003: Figure 3) analyzed a large variety of skeletal variants, and through cluster analysis created a tree diagram that grouped the world's major human populations according to the appearance of the skeletal traits used in the study. This particular study is perhaps the clearest application of the phenetic analysis of human groups in recent years.

While operational taxonomic units can be any sort of character, practitioners often choose very different OTU's that can possibly give different pictures of possible biological relationships between groups. Therefore a comparison of the results of the

clustering of different types of data is used to corroborate ideas of biological relationship between groups. For instance, there has been some debate about whether metric or nonmetric traits provide better evidence of biological relationship, as there can be different results based on the type of data used (Saunders, 1978). Often different samples will yield different results based on the type of character used in the estimation of biological distance (e.g. Pardoe, 1991). Other studies not only use different classes of skeletal data, but also compare completely different types of data to try to clarify the picture of genetic isolation and flow, and migration in different parts of the world (Barbujani and Sokal, 1990; Sokal, 1988; Sokal et al., 1986). In these studies, linguistic, geographical, and anatomical distances are used as data for a phenetic analysis to corroborate ideas about migration and biological relationships between human populations. These phenetic relationships are determined by the comparison of resemblance matrices, or the "S ←→S" procedures (Figure 3.1) as described in Sokal (1986).

The multivariate statistical methods used in biodistance, such as MMD, are model-bound approaches because they begin with the groups that will be studied already defined. Some researchers suggest that model free-approaches, such as wombling (Konigsberg and Buikstra, 1995), are better statistical tools than the model bound approaches which they relegate to heuristic procedures in biodistance analysis (Powell and Neves, 1999). The use of model-free approaches is based on the ordination of phenetic distances (Powell and Neves, 1999). Numerical taxonomy, therefore, could be considered the foundation for the model-free approaches used in biodistance analysis. The use of statistical analyses in phenetics and the post hoc

interpretation of the results is exactly what both physical anthropologists and pheneticists do in their analyses.

3.3.3 Phenetics and physical anthropology

Phenetics was developed and is used for the reconstruction of phylogenies, which must include data from both extinct and extant taxa. While anthropologists do not claim to be reconstructing a phylogeny (Howells, 1984), they do use dendrograms to illustrate the biological distance between groups. Phenetics has generally been treated as background knowledge in physical anthropology, and multivariate statistical analysis is generally taken for granted as a necessity (Pietrusewsky, 2000). The acceptance and use of phenetic methods has been somewhat naive. Moreover, although the early univariate analyses, such as the cranial index, were designed to construct a racial typology (Pietrusewsky, 2000), current multivariate analyses do not offer a much better alternative given their application.

Multivariate statistical analyses, and thus also clustering analysis, require that the groups to which individuals are assigned are determined a priori (Pietrusewsky, 2000). The definition and the assignation of groups before any analysis is similar to the racial typology of early physical anthropology, such as in the classification of different Native American groups by Georg Neumann. While the assignment of an individual specimen to a specific group is no longer as simple as general trait descriptions – for instance, Neumann often assigned descriptors like “more gracile” to Native American groups, in this case, specifically, Iswanid (Neumann, 1952) – the groups are still defined before any analysis of the bones begins. Although physical anthropologists state that racial

typology is no longer a guiding idea in skeletal analysis (Pietrusewsky, 2000; Szathmary, 1985), there is an exception in forensic anthropology with the use of racial categories in referencing the possible ancestry of an individual.

In the construction of a phenetic taxonomy, one criterion used to determine if the classification adequately represents the observed relationships between the characters used in the analysis is the predictive value of the analysis (Sokal, 1986). One of the characteristics of statistics is that they are used to predict the outcome of specific events within a certain margin of error. Anyone familiar with the election process has some familiarity with this aspect of statistical use. Pheneticists are not using prediction in the sense that the homogeneity of a particular taxon could ultimately yield the prediction of a yet-to-be-discovered trait, or predict the appearance of a undiscovered member of the given taxon. Predictability in this sense is used only to make a statement about the particular characters of a given taxon (Sokal, 1986).

The goal of biodistance analysis is a reconstruction of proposed genetic relationships between different groups of people. From this reconstruction, hypotheses are presented on how differences in biology reflect migratory patterns, significant population isolation, or even gene flow between populations. This, of course depends on the assumption that the frequencies of alleles of characters can be calculated, and used, in the sense of the population geneticists, to determine that some sort of evolutionary activity is happening, such as gene flow or genetic drift. Discoveries about the genetic control of the development of the overall pattern of the soma and anatomical characters raise serious questions regarding the appropriateness of assuming an allele

frequency basis for understanding differences between different species or subspecific groups.

3.4 PHENETIC ANALYSIS AND ITS USEFULNESS IN ANTHROPOLOGICAL RESEARCH

While phenetics has been broadly accepted in physical anthropology as the theoretical and methodological foundation for biodistance analysis, phenetics is not as widely accepted in the paleontology community where it started. Many systematists argue that phenetics is not a scientifically sound means of phylogenetic reconstruction, and that there are alternatives, such as cladistics, that are more appropriate. In fact, there has been an ongoing and often acrimonious debate within the systematic community about the best methods for reconstructing phylogeny (Funk, 2001; Hull, 1985).

Anthropologists generally have not acknowledged this critical debate within systematics. Indeed, it is standard for biodistance studies to use phenetics-based methods without acknowledging that they are using phenetics, although there are exceptions (Pietrusewsky, 2000; Powell and Neves, 1999). Taking for granted that phenetics is the appropriate foundation for biodistance analysis, anthropologists seem to be unaware that philosophers of science have repeatedly demonstrated that phenetics cannot withstand their critical challenges. These challenges address the most basic assumptions of phenetics, and, therefore, present a challenge to the methods of human biodistance analysis. There also seems to be some confusion about the use of cladistic methods. While unique characters should be used, determining the

average similarity of unique characters still constitutes phenetic analysis (e.g. Corruccini, 2001), and still reflects the problems of phenetic analysis.

3.4.1 Logical problems of phenetic analysis

There are two general lines of reasoning scientists follow to support a theory – a Baconian (verificationist/inductive) or a Popperian (falsificationist/hypotheticodeductive) method (Gaffney, 1979). The differences between these two basic approaches in science is best summed by Siddall and Kluge (1997:314):

> Verification uses what Popper (1983) called the "mistaken solution of the problem of induction" by seeking the "induced hypothesis" with the highest probability and in which a probability of 1.00 would be certainty. In contrast, falsification seeks the hypothesis that best survives the severity of test offered by the data, that is, the most corroborated hypothesis.

In other words, verificationists, in phylogenetics, are looking to statistics to determine the characters that are important in phylogenetic reconstruction (Frost and Kluge, 1994), and to determine the most likely scenario of evolutionary relationships (Siddal and Kluge, 1997). The current incarnation of verificationist philosophy in phylogenetic study is that of maximum likelihood methods, where frequency probabilities used to infer phylogenetic relationships, whether by common clades from different data sets, frequency of homoplasy, statistical confidence of phylogenetic hypotheses, or allelic frequencies (for an opposing opinion see Kitts, 1977; Siddal and Kluge, 1997). For physical anthropologists, this means that a test of the null hypothesis

is a test of the variability in one sample – whether the variation is the same or significantly different than found in the reference sample (Peterson, 2000; Sjøvold, 1973).

The adoption of phenetics/statistics/probability analysis by physical anthropologists is meant to make analysis more scientific. However, using statistical analysis to determine differences, if any, in the variation of skeletal traits does not necessarily make research more scientifically rigorous. Science is not simply the statistical study of accumulated data and the resulting degrees of probability. The falsification of hypotheses and the study of the problems of science that makes research scientific (Gaffney, 1979; Kluge, 2001b). This emphasis on the hypothesis and its corroboration are the lynchpins of scientific inquiry (Kluge, 1999; Kluge, 2001b).

It could be argued, therefore, that with the current use of phenetic theory to frame their work, physical anthropologists are falling into an inductive trap. In an a priori character analysis, whether in systematics or in biodistance analysis, the quality or "robustness" of the analysis depends on the number of independent tests of the hypothesis. The more tests pursued in which the hypothesis remains unfalsified, the more the hypothesis is corroborated. Tests of similarity and probability are really just one test, with many samples added on (Kluge, 2003b). Pooling more and more samples, and larger samples, moves the analysis farther away from the falsification needed for a historical science, placing analysis in a state of nonfalsifiability (Nelson, 1979). Although used over and over again in systematic analysis, the argument has been made that this enumerative induction intrinsic to phenetic analysis – the construction of inference from the "repeatedly observed to the unobserved" – has yet to

be justified as a reasonable means of phylogenetic reconstruction (Kluge, 2001a:200; Siddal and Kluge, 1997).

Overall, little seems to have changed in the use of phenetic analysis in physical anthropology, except in the tweaking of the specific statistical procedures. Perhaps physical anthropologists have been seduced by the elegance of statistics, and the feeling of being truly "scientific" they give. Statistics are certainly useful, but are not necessarily universally applicable. Physical anthropologists must be aware of the questions and of the subtleties of the questions that they are asking.

3.4.2 The assumption of similarity

Another problem with phenetic methods is the assumption that estimating or reconstructing biological/evolutionary relationships by the probability of overall similarity is the best means of scientific examination of any relationship between groups, species or otherwise. This is not the case. Collateral evolutionary relatives can resemble each other more so than they do descendant or ancestral evolutionary relatives. Simply being morphologically similar cannot be used to determine closeness of evolutionary relationship (Valentine, 2004).

The only factual outcome for probability analysis is that one form is likely to be similar to another form. This does not mean that the phenotypes are more likely to be similar to each other. The result is just a measure of similarity coupled with the assumption, which has been made beforehand, that similarity reflects common ancestry. These probabilities do not take into account the possibility of what systematists call *homoplasy*, where traits apparently shared between organisms are not

indicative of common ancestry. In cases of homoplasy, the characters used to demonstrate similarity actually have different origins (Kluge, 1999). Phenetic methods, therefore, cannot account for the possibility that degrees of similarity may not reflect relatedness. On the other hand, cladistics, as a hypothetico-deductive approach, does not make the assumption that seemingly similar characters reflect a biological relationship. Many systematists who use cladistics think that the possible *relationship* should be tested, not the similarity; biological affinity should not simply be assumed among organisms that appear to have a high degree of similarity (Kluge, 2003a; for an alternate view of cladistics, see Nelson, 1979; Nelson, 1989).

There are many questions about the use of phenetics in systematics, those physical anthropologists who use phenetics in osteological analysis must rethink their theoretical approach. A hypothetico-deductive approach borrowed from cladistics may be an answer to these problems. While cladistic hypotheses may not be falsifiable in the universal sense, they are testable (Hull, 1999). A move by physical anthropologists toward testing specific hypotheses about unique events in the past can put the discipline on a more logically solid foundation.

3.5 AN ALTERNATIVE APPROACH

Since the adoption of phenetic methods by physical anthropologists in the 1970's, the importance of the theoretical debate in systematics between pheneticists and those who support alternative methods, such as cladistics, seems to have escaped the notice of physical anthropologists. Specifically, human osteologists and skeletal

biologists have not reviewed the problems of the inductive, Baconian approach offered by phenetics. The assumptions and their burden on phenetic analysis indicate that an alternative means of phylogenetic reconstruction. Coupled with the misperceptions of the nature of DNA and its evolutionary significance, the consequences of the assumptions on which phenetic analysis relies is that the classification and ordering of taxa is removed from biological reality to an unacceptable degree.

Biodistance analysis shares the burden of these assumptions with phenetics because of their common logical foundation. There is a need, therefore, in biodistance studies for methods not based on phenetics. A preferred method would be one that would not have to rely on the assumptions required by phenetics and biodistance methods. Cladistics, as a hypotheticodeductive approach, is an appropriate foundation for an alternative to current methods in biodistance analysis. An approach to biodistance based in cladistic methods instead of phenetics would need not rely on as many assumptions as phenetic analysis, and therefore be less vulnerable to logical problems such as circular arguments. Cladistics, because of its foundation in Popperian hypothesis testing, represents a means of circumventing the problems of statistical analysis in biodistance, such as the model-bound and model-free approaches, and need not rely on a precise understanding of exactly how genes control the development of specific anatomical characters.

4.0 CLADISTICS AND CHARACTER CHOICE

4.1 INTRODUCTION

When analyzing and comparing the morphology of different human groups, the comparison is, by definition, intraspecific. For many systematists who study intraspecfic groups within nonhuman species, phenetic analysis and the use of probability in determining the differences in variability are the keys to coming to a satisfactory conclusion (Wiens, 1999). It is therefore not surprising that anthropologists who compare groups of humans use methods based on phenetic analysis (Powell and Neves, 1999).

The classification of groups or taxa is not simply a matter of assigning convenient labels to categorize biological units, evolutionary patterns, or organisms. Any statement of classification is a statement supporting a specific theory of evolutionary relationship (Kluge and Wolf, 1993). There are objections to the idea that anthropologists are in some way reconstructing a phylogeny (Howells, 1984; Weiss, 1985). Because organismal change through time is explained by evolution, it is difficult to perceive biodistance analysis as anything but an attempt at reconstructing phylogeny at the subspecific level through measured similarity. The methods of phenetics cannot be decoupled from the theory on which they are based; that evolution is a statistical

process and phenetic methods illuminate evolutionary relationships (Sneath and Sokal, 1973; Sokal and Rohlf, 1969).

Although phenetics and probability analysis have been applied to systematics and to biodistance expressly to satisfy the perceived need to make both disciplines more scientific (Hull, 1985), one does not have to employ probability analysis to be scientific. The general scientific theories and methods developed by Karl Popper provide a logical, hypothetico-deductive framework for testing hypotheses, without the need for reliance on degrees of probability (Kluge, 2001b). As Kluge (1997) states:

> Scientists do not actually seek the truth, because truth is unknowable. Scientists do, however, attempt to approach some unattainable objective truth, and do so by critically evaluating different explanations. Hypotheses can never be proven true, as inductivists seek to do, nor be proven false, as deductivists claim to be able to do; they can be found to be more or less corroborated; the others do not. This is science according to Karl Popper.

Hypothetico-deductive methods, and not inductive methods, should serve as the framework for the examination of any evolutionary/biological relationship. The most distinct reason is that cladistics has greater explanatory power over phenetics, because phenetics puts similarity before phylogenetic reconstruction, which is like "putting the cart before the horse" (Siddal and Kluge, 1997:329). A hypothesis about relationship should first be constructed, and then tested (Kluge, 2003b; Siddal and Kluge, 1997). The foundation of testability in cladistics is not probability, but refutation and corroboration through the testing of alternative hypotheses (Kluge, 1997). Anthropologists should continue to look to systematics for methodological and theoretical guidance to avoid improper scoring and vague descriptions of important

characters (Saunders, 1989); but cladistics, and not phenetics, should be the methodological focus for biodistance analysis.

4.2 CLADISTICS

A taxonomic theory is presented with the assumption that evolution is the overall framework of differences found in biology. But for any theory to be genuinely useful, it must be judged on its usefulness in explaining natural phenomena (Kluge and Wolf, 1993). To arrive at a reasonable reflection of the natural world, scientists must test and retest hypotheses, and those hypotheses that are the most corroborated represent the closest approximation to reality. Although there are many pitfalls in formulating hypotheses, those that seem to burden systematic classification are assumptions (Forey, 1982) and the inappropriate application of statistical methods to a historical science (Frost and Kluge, 1994). Although Forey's (1982) criticism that assumptions separate a hypothesis farther from reality was leveled specifically at the evolutionary systematics of Mayr (1969) and Bock (1974; also Mayr and Bock, 2002), his basic logic holds for any method of deriving theories in systematics.

Systematists are not only reconstructing evolutionary relationships, they are also reconstructing past events and recovering this history (Frost and Kluge, 1994). History is unique, with specific events requiring explanation, not estimation or prediction (Kluge, 1997; Siddal and Kluge, 1997). Prediction and estimation are excellent and powerful tools for the examination of universals and making inferences regarding historical

generalities, but not the historical particulars of phylogenetic reconstruction (Siddal and Kluge, 1997).

Systematists use “species” as the focus of phylogenetic reconstruction. There is general agreement among systematists that the species is the only real biological unit in nature and thus used for evolutionary study (Schwartz, 1999a). Speciation events, therefore, are the critical historical, spatiotemporally constrained occurrences represented by character transformations that are explained by systematists (Grant and Kluge, 2003). These speciation events cannot be directly observed, making the formulation and testing of historical hypotheses the only acceptable means of reconstructing these historical events and explaining the evolutionary relationships between organisms. “It is clear… that cladistics is *the* general method of historical science” (Rosen et al., 1999:X). Cladistics can be used to uncover hierarchical relationships among groups of organisms as long as evolutionary change occurs as modification through decent (Hull, 1979; Platnick, 1979; Siddal and Kluge, 1997). Indeed, there is no reason to compare hierarchical characters that are not related evolutionarily, as their “origins, functions, and fates are not necessarily the same” (Kluge, 2001a:199).

Systematics, like aspects of physical anthropology, is, therefore, a historical science focused on searching for explanations, not predictions. Statistical probability in systematics, such as a verificationist-inductive approach, does not provide explanation (Siddal and Kluge, 1997). Where statistical analysis seeks to estimate and predict outcomes, games of chance, for instance (Kluge, 2001b; Siddal and Kluge, 1997). Probability is applicable, therefore, in the search for generalities, and specifically, in the

case of the sciences, for universals (Frost and Kluge, 1994; Kluge, 1999; Kluge, 2003a; Siddal and Kluge, 1997). Phylogenetic reconstruction is *retrodicting* (or *postdicting*), and cladists argue that phenetic methods are an inappropriate framework to evaluate historical hypotheses and therefore need explanations because evolutionary changes represent past events (Frost and Kluge, 1994; Siddal and Kluge, 1997). Classifications are not statements of generalities or universals; they are organizations of past instances.

4.2.1 Cladistic methods of phylogenetic reconstruction

Biological classification, at any level, represents a theory or a set of theories about the biological relationships of specific groups (Farris and Kluge, 1986; Kluge and Wolf, 1993). In a hypothetico-deductive framework each classification represents a hypothesis that should be tested against competing hypotheses (Jenner, 2003). Each group delineated in a cladistic analysis is defined by a set of unique, derived anatomical traits. The hypothesis that is established for testing need that only a member of the particular group defined will have these specific characters. Using deductive methods afford scientists the ability to choose among alternative empirical hypotheses (Kluge, 2003a).

The testing of hypotheses of classification in systematics by testing one hypothesis against others was introduced by Hennig in *Phylogenetic Systematics* (1966). Hennig detailed an analytical program for phylogenetic reconstruction that uses hypothetico-deductive methodology by which competing hypotheses can be tested and either refuted or supported. The set of methods developed by Hennig and now refined

by other systematists (Cracraft, 1978; Eldredge and Cracraft, 1980; Kluge, 1999; Siddal and Kluge, 1997) is now known as cladistics or cladism, although the moniker was not coined by Hennig, but by his early critics (Hull, 1979; Mayr, 1969). In his monograph, Hennig wanted to establish a truly historical approach to systematics (Knox, 1998). He also wanted to establish systematics as a science. This is not to say that evolutionary studies were not considered a science at the time, but morphological or typological systematics lacked a rigorous theoretical framework (Richter and Meier, 1994).

Hypothetico-deductive reasoning has become associated with the philosopher of science, Sir Karl Popper (Hull 1999, Gaffney 1979, Kluge 1999). The hypothetico-deductive (deductive) approach, arguments offers scientists a rational, objective choice among hypotheses (Kluge, 2003a; Siddal and Kluge, 1997), which stands in direct opposition and as a serious challenge to the inductive, probabalistic approach favored by the majority of physical anthropologists.

Although Hennig did not cite Popper in his seminal work, the relationship of their respective philosophies of science has become important in systematics. If Hennig did not cite Popper in his masterwork, why is it important that Popper is invoked by latter-day cladists? It is because phylogenetics is an historical endeavor, and a deductive model is necessary for historical explanation (Kluge 1999). As the 20th century's most notable deductive philosopher of science, Popper (1980) directly commented on the scientific method in the reconstruction of phylogenies. And if one accepts that "Hume's (1739) challenge has never been met" (Siddal and Kluge, 1997:318), deduction remains as the only viable scientific means to the historical reconstruction of biological relatedness (Kluge, 1999). Popperian testability – the *attempt to falsify hypotheses* – is,

according to cladists, the key to phylogenetic reconstruction. Strictly speaking, however, universal laws are falsifiable; evolutionary statements are singular and only testable (Hull, 1999). Testability of phylogenetic hypotheses is all that is required, because systematists are not evaluating *how* evolution happens (process), but *what* happened in the course of evolution (Hull, 1999). The process of evolution is universal, but the mode of evolution is still debated by scientists and is effectively not testable. What *happened* as a result of evolutionary change is recorded in the biology of extant organisms and in the fossil record. This information constitutes empirical evidence of decent with modification and ancestor/descendant evolutionary relationships. Cladists are not attempting to falsify in the sense of these types of universal natural laws – they are not testing the various hypotheses of the mode of evolution. But they repeatedly test alternative hypotheses formulated on empirical data against competing hypotheses, which leads to strengthening the corroboration of the most parsimonious hypothesis (Kluge, 1997; Kluge, 1999; Kluge, 2003a).

Siddall and Kluge (1997:330) specify the type of testability used in cladistic analysis as "sophisticated falsification." The keys to sophisticated falsification are competing hypotheses, a high amount of empirical content, and an accumulation of corroboration (Kluge, 1999; Siddal and Kluge, 1997). Practically, testing only works when statements are formulated as phylogenetic hypotheses, and shared, derived characters are considered as prospective contesting evidence (Kluge, 2001a). Thus historical reconstruction can be tested within a hypothetico-deductive framework (Kluge, 1999).

A deductive model of the explanation of past events would be as follows (after Kluge, 1999; Kluge, 2001a):

L – explaining laws
C – specific initial conditions (cause)
_____ explanation
E – specific event (end effect)

To apply this model to cladistics would yield the following:

L – descent, with modification
C – cladogram
_____ explanation (of inheritance)
E – synapomorphy (as homology)

Descent, with modification can be taken as part of the background knowledge, a necessary assumption for any model of evolutionary change. A hypothesis would be written as representing the initial condition of biological relationships for the particular hypothesis to be formulated and tested. The hypothesis formulated is an attempt to explain the appearance of shared, derived traits, and thus the biological relationships found between organisms.

4.2.2 Homology and Synapomorphy

A concept of utmost importance to cladistic analysis is that of homology. The comparison of hierarchically arranged, homologous structures is the foundation of comparative biology, and pervades all hierarchical levels of biological organization

(Fortey and Jefferies, 1982; Hall, 1994). For such an important and all-encompassing concept, the exact definition of homology is difficult to articulate (Wagner, 1989). A basic, and useful, definition of homology is that the intrinsic nature of a given biological character in one organism is the same in another organism; or, alternatively, that the character found in the first organism is derived from the same ancestral form of the character as the character found in the second organism. Such characters are called *homologs*. The ancestral form of character would also be found in a hypothetical ancestor for the organisms sharing homologues (Nelson, 1994).

Concepts of homology have historically been applied exclusively to morphological characters (Mayr, 1982; Panchen, 1994). Geneticists, however, have argued that homologues can be found in molecular characters. Molecular analysis tends to be phenetic in theory and method, with conclusions based on similarity and stated in quantified relationships where particular genes are homologous to a specific percentage (Hillis, 1994). Another alternative application of the homology concept is to the homology of developmental pathways and developmental constraints (Roth, 1988; Roth, 1994; Wagner, 1994). Homologies of developmental processes, however, are useful only in bridging the gap between biological comparisons of genetic and morphological characters in phylogenetic reconstruction (Gilbert and Bolker, 2001). In this way homology may be useful in regard to the continued understanding of how developmental genetics controls the appearance of the phenotype.

For the majority of systematists, homologous phenotypic structures represent the majority of data used in phylogenetic reconstruction. Cladistics, therefore, illuminates a hierarchical arrangement of homology as well as reconstructing phylogenies and

speciation events. Organisms are arranged in nature in a nested hierarchy of relatedness (Valentine, 2004). The hierarchical structure of the evolutionary relationships of taxa is not a reification of a hypothesis. Throughout the complex biological world, entities are grouped into hierarchies, which are nested in their structure (Goldstein and DeSalle, 2000; Valentine, 2004). The overarching biological hierarchy is "an objective property of the living world," demonstrated by the shared homologous structures between organisms (Nelson, 1994). In fact, according to Nelson (1994:109):

> Homology is phylogenetic relationship between parts of different organisms, as indicated for example by the tree (cladogram) relating the organisms themselves. Taxon and homology are the same phylogenetic relationship, as seen either between organisms (taxon) or between their parts (homology).

One needs homology to reconstruct phylogeny, but they are not equivalent. Homology does not explain common ancestry; common ancestry is the cause, and therefore underlies, the phenomenon of homology (Kluge, 2003a).

By definition, tests of alternative phylogenetic hypotheses consist of the evaluation of possible synapomorphies, not autapomophies or symplesiomorhpies (Kluge, 2003a). *Synapomorphies* are homologies that illuminate a shared evolutionary past (Frost and Kluge, 1994). Synapomorphies are characters that are shared by related groups, revealing their common ancestry and thus are homologous structures (Ashlock, 1974; Cracraft, 1982; Hennig, 1966; Kluge, 2003a). Synapomorphies, therefore, are the only characters that can be used as tests of phylogenetic hypotheses. *Autapomorphies* are derived characters unique to a particular group, associated with monophyletic groups, most notably species. These characters cannot by their nature

be shared by more than one group, and are therefore not useful in testing biological relatedness. *Symplesiomorphies* are primitive characters shared by many groups, thereby giving no information as to the closeness of biological relatedness of groups, except in their juxtaposition to synapomorphies. Symplesiomorphies are not derived, but primitive traits shared among many groups. Only unique, shared traits present data that can be used to illuminate evolutionary historical relationships (Kluge, 2003a).

4.2.3 Cladistic hypothesis formulation

Phylogenetic hypotheses created from Hennegian methods are represented by trees of relationships, but not the tree diagrams that graphically illustrate the results of a phenetic analysis (Valentine, 2004). Trees constructed cladistically represent the hierarchical branching of evolutionary relationships, which are represented in *cladograms* – diagrams of nested ranks indicating shared uniqueness in character (Figure 4.1). A cladogram is a phylogenetic hypothesis. Alternative cladograms of the same taxa represent alternative hypotheses to be tested against each other. The preferred alternative hypothesis is the most parsimonious hypothesis that requires the fewest number of evolutionary steps (Siddal and Kluge, 1997; Valentine, 2004). Cladistics, however, should not be simply equated with parsimony analysis and a search for hierarchy, as some researchers claim (Lee, 2002). But because a hierarchical arrangement is intrinsic to biology (Nelson, 1994), cladistics relies on parsimony to choose among competing hypotheses to illuminate the hierarchical arrangement of evolutionary relationships (Brower, 2002; Kluge, 2001a; Knox, 1998).

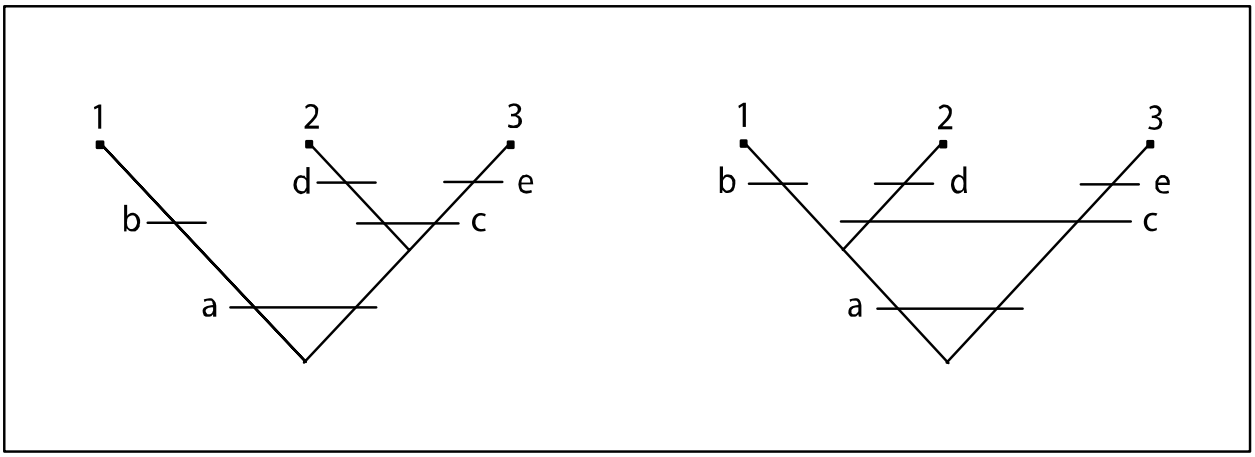


Figure 4.1: Cladograms representing competing hypotheses of relatedness.

For example, Figure 4.1 shows two cladograms, each representing an alternative hypothesis. Cladogram 1 shows the more parsimonious of the two alternatives, and is thus the more supported of the two hypothesized schemes of biological relatedness. The three groups represented in the cladograms as 1, 2, and 3 are all united by the shared derived trait (synapomorphy) "a." Groups 2 and 3 are united by the synapomorphy "c," and the traits "b," "d," and "e" are autapomorphies delineating each terminal group as monophyletic (individual, unique groups such as species). Several assumptions must be made in order to accept Cladogram 2 as representing genuine biological relationships. In order to accept this hypothesis, the assumption must be made that the character that unites groups 1 and 2 has been lost in evolutionary history, making those groups appear not to be related when in truth they are. In any hypothetico-deductive analysis, the hypothesis that contains the least amount of assumptions and therefore stands up to the most rigorous of repeated challenges is the most corroborated, and thus the most supported, hypothesis (Grant and Kluge, 2003; Siddal and Kluge, 1997).

4.2.4 Problems of identification of biological human groups through morphological analysis

There are two general problems in the application of current biodistance analysis: the analytical methods are phenetic and the grounding in population genetics are untested assumptions. There is an alternative that has not been explored by anthropologists outside of paleoanthropology: cladistics. Although historically specific events like evolutionary relatedness can never be known, a deductive approach ensures a logically sound way of getting as close to the reality of evolutionary history as can reasonably be expected. In order to overcome the problems presented by currently used methods in biodistance analysis, physical anthropologists must turn to cladistics to provide a theoretical foundation on which to build biologically real biodistance studies.

Perhaps there is a difference between the questions that are typically being asked in physical anthropology, and those we should be asking. Indeed, what are we interested in learning? For studies in biodistance, the proximate goal is to determine the biological distance between individuals or groups. But ultimately osteologists and archaeologists want to determine past events, such as migration, matrilineal patterns, and endogamy/exogamy. What has been acknowledged or recognized by physical anthropologists, is that they are using the same kind of evidence and similar data that is the bread and butter of systematists, who are also reconstructing past events, although they are specifically evolutionary (speciation) events. Fossils, for instance, have the only surviving indicators of biological relationships of organisms in their morphology, whether the evidence is qualified or quantified in terms of size, shape or dimension.

The concepts currently used to determine biodistance are based on methods most often associated with phenetics. Phenetics is the Gestalt of overall similarity of identifiable or measurable characters revealing probable evolutionary relationships between extant and extinct organisms. The overall concept of phenetics is that the results of an analysis of a given sample will yield an average, of whatever character presence or measurement, and their average is compared to averages of other samples. These statistics have come to represent the sample, and to represent a significant, if not *the* significant character of the represented population. This system relies on samples and populations that must be defined previously and used as *a priori* knowledge to apply a statistical analysis to the differences in central tendencies of the different samples. The amount of difference between the averages is regarded as the generalized biological distance between populations.

In general, the characters of human skeletal material are not placed in an evolutionary context. That is, the characters are only considered in terms of the frequency of their appearance; they are used in biodistance analysis regardless of their etiology. This sort of reasoning puts the cart before the horse. The boundaries of the population are usually defined by traditional means, either by general geography or by long-standing assumptions of the biological histories of populations. These assumptions, however, are the very ideas that should be tested, not relied upon as a given factor in biodistance analysis. If skeletal characters can be used to determine the genetic relationships of different groups of extinct and extant peoples, they should first be used to determine if a given sample is comprised of individuals who are genetically related.

The crux of this project is to try and determine if nonmetric skeletal characters can be used to determine if individuals within a sample are indeed all related. One would presume that if characters can be used to determine differences between groups, they can be used to determine if the individuals in a sample are representative of a genetically identifiable population.

Analyses based in phenetics are woefully inadequate to accomplish this task. The characters historically and currently used in nonmetric analyses are found in all groups of humans, and therefore provide no information about what would be unique to a population in order to delineate that population with any degree of certainty. An cladistic analysis offers an opportunity to test hypotheses about the biological nature of a human skeletal sample.

4.2.5 Cladistics and Biodistance analysis

While the authors of the forward to the reprint of *Phylogenetic Systematics* may not have thought of the application of cladistics beyond tokogenetically related groups (species) (Hennig, 1966), phylogenetic systematics can be applied to all levels of the analysis of biological relationships (Kluge, 2003b). Cladistics offers the ability to test hypotheses of biological relationships, regardless of the analytical/hierarchical level (Kluge, 2003b), including the intraspecific level. Biodistance or any other analysis of different human groups constitutes an intraspecific level of analysis. Since intraspecific groups of any sort are a part of a general biological hierarchy (Goldstein and DeSalle, 2000), I would argue that because cladistics is the most appropriate means of illuminating the hierarchical, evolutionary relationships between organisms, it is also the

most appropriate means of comparing human groups. As such, cladistics, not phenetics, should be the foundation for biodistance analysis.

A significant aspect of the deductive logic of cladistics is that it assumes very little about how biological change occurs. Cladistics does not assume rates or modes of evolutionary change or amounts of homoplasy, and does not require results to be probable or likely. Cladistics assumes that character distribution is historically contingent and only requires that "the preferred hypothesis be better corroborated by the data than the alternatives; that the explanation explains the explanans" (Siddal and Kluge, 1997). In other words, cladistic methods do not rely on any given model of trait inheritance, of genetic instruction, or of natural selection. Therefore, debates about genetic control over traits, whether a trait is epigenetic, or the heritability of traits become moot. All that matters is that the preferred hypothesis of biological relationship is more highly corroborated than competing hypotheses, and thus has more explanatory power (Kluge, 2003a). For biodistance analysis, this means that the hypotheses of relationships between groups need not rely on models of any kind, or the likelihood of any particular relationship; only that they are tested and corroborated against alternative hypotheses.

4.2.6 Outgroup comparison

Although not part of Hennig's vision of systematic methods (Richter and Meier, 1994), today one of the more overlooked aspects of cladistic analysis is outgroup comparison (Cracraft, 1982; Eldredge and Cracraft, 1980; Gaffney, 1979; Kluge, 1997; Kluge and Wolf, 1993). Outgroup comparison allows cladists to gauge the uniqueness of a

particular group. The comparison is relatively simple – if the traits used to formulate the hypothesis that one group is unique are found in another group, the conclusion can only be made that those traits do not constitute evidence of a homogenous group. The hypothesis of biological relationships put forth by the cladist is, therefore, not corroborated.

Cladistic methods have been used in biodistance analysis. Stringer et al. (1997) re-evaluated the use of major dental characters in the delineation of general populations of humans, specifically the characters that make the morphological patterns which are commonly called Sinodonty and Sundadonty (Scott and Turner II, 1997; Turner II, 1990; Turner II, 1992). Sinodonty has been hypothetically associated with Asian and Native American populations, and Sundadonty with Southeast Asians and is also hypothesized to be the dental pattern most like the human ancestral form (Turner II, 1990).

Stringer at al. (1997) correctly point out that the methods used for these dental analyses rely on frequencies of averages; they are measures of phenetic similarity, even if presented in tree diagrams labeled cladograms (also see Schwartz, 1995; Schwartz and Brauer, 1990). Stringer at al. (1997) include outgroups in their re-evaluation of the patterns of Sunadonty and Sinodonty, specifically samples of *Homo neanderthalensis*. Trait analysis in biodistance should focus on uniqueness, not on the frequency of commonly occurring dental characters (Scott and Turner II, 1997), skeletal morphology or measurements (Howells, 1995) to argue for phenetic similarity (Schwartz, 1995).

By including a non-human hominoid in the comparisons, the authors were able to determine that similarities in dental features are due to symplesiomorphies and not

synapomorphies. The traits used in biodistance are rarely, if ever, seen as possibly existing beyond human anatomy, whether in hominids or other hominoids. By not considering the appearance of nonmetric traits used in human biodistance analysis, physical anthropologists have placed humans outside of the framework of the biological hierarchy. This practice is anathema to comparative analysis in biology, and in cladistics specifically. Anthropologists should consider the possibility that skeletal characters used in comparative studies in humans may also be found in other, closely related organisms.

4.3 CHARACTER CHOICE

Given the different choices of traits made by various researchers (Table 2.1), the skeletal traits chosen for use in a comparative biodistance study become an important point in skeletal analysis. First, the number of characters appropriate for the study must be determined. Some studies test to see if the variability of one or two traits can tell us about the relationships of a small number of specific groups, or even between families (Saunders and Popovich, 1978). Studies that compare large populations generally use a varying number of different standardized traits (Buikstra and Ubelaker, 1994; Larsen, 1997). As long as the appropriate traits are chosen for the hypothesis to be tested, no problem should be encountered with the number of different traits used. The realities of research often means that the limits of how large skeletal and trait samples that can be obtained are time, money, and the availability of the necessary samples.

For phenetic analysis of biodistance, variation in the frequency of expression between different groups is the key to determining biodistance. But some variation in the expression of characters is not related to the overall group, but the specific individual's idiosyncratic characters. Variability in expression may be due to biological factors such as sex and age (Saunders, 1978). Many of these characters appear to be related to the difference in robusticity due to sexual dimorphism. Another factor that may contribute to these differences is differences in activity between the sexes. Some studies of nonmetric traits include occupational stress markers – places on the bone that have been remodeled due to the stress of a repeated activity. Squatting facets, for instance, have been used in trait lists (Finnegan, 1978). Squatting facets are the result of the hyperflexion of the knees, ankles, and toes due to maintaining a prolonged squatting position, and are often associated with agricultural activities (Schwartz, 1995). The use or the disuse of particular parts of the skeleton can cause changes in the bone like the squatting facets, increased and decreased rugosity of muscle markings, and increased skeletal mass or the atrophy of bone. These kinds of traits are not developmentally based or genetically controlled. They are, therefore, not useful for any sort of hypothetico-deductive analysis. In years past these traits have been used in biodistance analysis (see Table 2.1), but because of their non-biological etiology, they should not have been.

Nonmetric traits can also appear on one side of the body, and not on the other. This asymmetry has been attributed to environmental factors, affecting the appearance of nonmetric traits (Trinkaus, 1978). Because of the highly variable appearance of these skeletal traits in individuals, they have very little information that can be useful for

biodistance analysis, although they may be used as data for researchers studying the interaction of bone and environmental influences.

In traditional biodistance analysis, when a particular trait is expressed in different forms in different individuals, it should be excluded from the study (Richtsmeier and McGrath, 1986). The number of times a trait appears in a given population or in humans in general may also affect its choice for biodistance study. If a trait is ubiquitous, it sheds no light on trait differences. In turn, a rare trait is of limited value in illuminating genetic differences (Conner, 1990). Presumably, if a trait is too rare, no central tendency can be measured because of the small sample results. Rare traits and different forms of trait expression, however, may yet hold information important in biodistance analysis.

5.0 METHODS AND SAMPLES

5.1 INTRODUCTION

The hypothesis-testing methods used here are grounded in cladistic analysis as is used in systematics for testing hypotheses of evolutionary relationships. Cladistics has the added advantage that it can also be used to test biological relationships without the burden of applying a label indicating a taxonomic level or relationship. This is critical because the study of human skeletal sample, is an analysis at the subspecific level. The methods used here begin with the assumptions that all samples studied represent either historic or prehistoric human populations, and that any differences found between the samples are simply examples of the diversity to be found throughout various human groups. The unique characters are derived, and could be considered hyper-derived for small subsets of population or species, including humans. The initial focus hypothesis development in a cladistic analysis is on primitive versus derived character states. Only after these character relationships have been tested and successfully can hypothesized evolutionary relationships be considered (Schwartz, 2005).

The samples of human skeletal material that were analyzed for this dissertation were chosen because of their applicability in addressing the specific hypotheses discussed earlier, as well as because of their availability and state of preservation. The primary sample used is the Spitalfields skeletal collection, which is housed at the

Natural History Museum (London). Several other samples were analyzed for purposes of comparison with the Spitalfields sample.

5.1.1 Trait choice and cladistics

Which specific types of anatomical characters should be chosen for analysis? An extensive knowledge of comparative anatomy, at least of the organisms to be studied, is essential in order to seek out unique forms of characters. Discrete, nonmetric traits are ideal candidates for the application of methods based on cladistics to human biodistance analysis. Skeletal collections can be easily examined for characters that appear to be unique to that particular sample.

The exclusion of traits that appear asymmetrically, the association of traits due to age, sex or activity, and the exclusion of rare or ubiquitous traits highlights the problems associated using nonmetric traits. Unique derived characters are needed to delineate related groups. If characters are not unique they cannot be useful in cladistic methods of analysis. Cladistics makes the decision of which traits to use in biodistance analysis relatively simple. In keeping with cladistic analysis, unique characters or unique forms of known nonmetric traits should be used.

5.2 SUMMARY OF METHODS

Cladistics provides the most scientifically logical foundation for the reconstruction of past biological events, specifically those events of genetic isolation and biological change. Cladistics is the most appropriate method for phylogenetic reconstruction by

systematists, and is therefore the best foundation for methods of determining biological relatedness in biodistance analysis.

Four steps need to be taken in order to answer the questions presented above. The first step is to choose the appropriate reference sample to establish the foundation for the comparative study. The best reference sample to test a hypothesis of human morphology and biodistance is one that consists of the skeletal remains of known individuals, preferably with some sort of familial relationships to substantiate genetic affinities. One sample fits these criteria very well: the Spitalfields Collection housed at the Natural History Museum (London). Samples with which to compare the results of the analysis Spitalfields sample were chosen based on the individuals represented, preservation of the skeletal material, and availability of the samples for study. The analysis of the human skeletal sample is discussed in the next chapter.

The second step in the analysis is heuristic. It is the discovery phase for the data to be used in research. For the construction of phylogenetic hypotheses an exploratory examination of samples to obtain an initial impression of the distribution of characters to be used in constructing the preferred hypothesis is necessary. Heuristic methods must be scientifically objective and data focused in order to formulate empirically founded hypotheses for appropriate deductive testing (Grant and Kluge, 2003). The hypotheses to be tested must come from the data. The type of data required must facilitate the empirical testing of hypotheses (Grant and Kluge, 2003). For human biodistance analysis, this means that the standard lists of traits commonly used should not be uncritically applied in cladistic analysis. Therefore, the traits used in an analysis should

exhibit a unique form, and possibly demonstrate the uniqueness of the population. One can only delineate characters by direct observation.

In this study the heuristic phase consists of a descriptive examination of the reference sample. I twice examined a large sample of the Spitalfields cranial material, which I focused on because of their relatively high frequency of evaluation and preservation. After the initial examination, a second examination was conducted to reaffirm possible traits that could be used in the analysis. Along with this second examination, brief descriptions of some of the potentially useful characters and the specimens themselves were recorded; photographs were also taken (Appendix F). From this initial exploratory phase, I constructed data sheets in order to record the presence and form of the characters for each individual in the sample. The examination and scoring of each individual in the sample was the basic step in the next phase of analysis.

The third phase of analysis is what systematists generally call “alpha taxonomy.” In phylogenetic reconstruction, alpha taxonomy is a description of the species of interest in the study. The formal definition of alpha taxonomy is that an “emphasis is on the description of new species and their preliminary arrangement in comprehensive genera” (Mayr, 1969) through the discovery, selection, delineation and resolution of morphological characters (Poe and Wiens, 2000; Thiele, 1993). This project is not concerned with variation, however, but with potential uniqueness. Therefore it is more appropriate to use alpha taxonomic methods to illuminate possible unique characters that would be the foundation of a cladistic analysis.

The easiest means of delineating these characters is recording them on a basic score sheet (e.g. Appendix A; see Chapter 6 for a complete explanation of skeletal traits). The scoring sheets created for this project are not the same as the lists used in a typical biodistance analysis. They are the result of the discovery phase for the reference sample. The traits may or may not be found in other samples. This is precisely what is to be tested. The possible unique characters or forms of characters chosen are, in part, based knowledge gained through study of what are typical morphological characters of the human skeleton. With this background knowledge, it is more likely that unique characters can then be illuminated. Photographs were also used extensively for subsequent comparisons of the characters between samples.

Scoring of characters also requires another examination of the sample. It thus offers another opportunity to discover traits that may be useful in the analysis. This pass through the sample was used to try and identify characters that might be used to delineate groups within the reference sample itself. This part of the analysis focused on answering the question of whether or not data can be uncovered that can demonstrate familial relationships within a sample. This would represent the lowest possible point in a hierarchy of biological relationships.

The final phase of analysis was to compare the data collected from the reference sample with other samples in order to test the hypothesis that at least some of the traits recorded in the analysis of the reference sample are indeed unique, i.e. indicate that the group is possibly a relatively isolated breeding unit. While this is the last step for this project, hypotheses of biological relatedness should always be tested in every biodistance analysis.

Through these comparative methods, I sought to determine if cladistic methods can be used in biodistance analysis, and if so, how low in the biological hierarchy at what level they are viable. Specifically, unique traits can be used to delineate morphs, which generally represent subspecific groups (Thain and Hickman, 1994). The term "morph" is equivalent to the older taxonomic terms "variety" and "phenon" (Stump, 2005). Contrary to some authorities (e.g. Wood, 2005), a morph is not the equivalent of an OTU used in phenetic analysis and, as such, is not operationalized. A morph is a unit of biological specimens, that when compared to a similar group of specimens, differs diagnostically in the appearance of specific, morphological characters (Stump, 2005). According to Mayr (1970), for example, the level of taxonomic comparison is a subspecies if the group is only geographically isolated, and a species if the group is both reproductively and geographically isolated (Stump, 2005).

The idea that a "morph" should be used to designate a distinguishable biological subgroup, an isolated breeding population within a species, was proposed by Edwards (1954). Edwards stated that morphs should not be given technical names as taxa, which is reasonable as they are considered neither subspecies nor any other level of taxon, species or otherwise (Simpson, 1961). It is, therefore, not necessary that a taxonomic rank be associated with a morph, only that the morph be distinguishable enough to be tested against other groups. Any taxonomic classification, or any other label, is an appellation to be given to a group of specimens based on the hypotheses of shared characters determined by the researcher.

If none of the traits used to formulate a hypothesis about relationships between and within groups can be regarded as unique, then the hypothesis of a morph based on

the presence of those characters must be rejected. If there are characters that appear to be unique to a given sample or subset within a sample, then the hypothesis of the group being a morph is corroborated. A morph need not be any particular taxonomic group or level, but a group of specimens that share common, derived traits. Any hypothesis of taxonomic relationships must come after establishing of a group as a morph.

The ultimate questions for this project, therefore, is can a morph be delineated from a sample of human skeletal material? If morphs can be delineated in human skeletal samples, then comparisons can be made to other samples in order to determine their morphological and, therefore, biological differences.

5.3 SAMPLES

5.3.1 Sample Choice

When testing methods of determining and hypotheses of biological relatedness of skeletal samples, it is best to use samples of individuals of known age, sex, and familial relationship (Richtsmeier and McGrath, 1986). There are only a few skeletal samples in the world for which this kind of detailed information is available. Therefore, in order to maximize the potential outcome of this investigation, two samples of known individuals were examined: the Spitalfields collection (Natural History Museum, London) the Terry Collection (Smithsonian Institution, Washington, D.C.).

Since the majority of specimens included in biodistance studies were recovered archaeologically and are often in less-than-good condition, with many elements missing

or destroyed by diagenic processes, it seemed reasonable to gauge the analysis of the Spitalfields collection against a collection of archaeological specimens. Consequently, two archaeological collections from North America were included in in this study. One sample is a protohistoric skeletal collection from a Monongahela site in Southwest Pennsylvania, and the other is a sample form an archaic site from the northwest corner of Alabama.

The focus of this study on the cranium was due in large part to the long tradition of documenting skeletal characters from the skull (Hauser and De Stefano, 1989), as well as time and preservation issues. The cranium is also different than the rest of the skeleton in development and form. The cranium also develops mostly from neural crest cells, and not cartilaginous replacement. It houses the brain, accommodates the cranial nerves and other important soft-tissue structures that vary in their development. Adult crania were the only ones examined in this study, and they were not divided into more specific analytical age groups. For the samples of known individuals, age was recorded as part of the individual profile. For the Monongahela sample, the determination of adulthood was made by noting the degree of cranial suture closure, epiphyseal closure, and dental development. Sex was determined when possible using standard morphological methods (Schwartz, 1995). The age and sex for the individuals of the Alabama sample had been previously determined and were on file at the University of Alabama.

The central hypothesis to be tested in this project is: Can unique traits be identified within a single group of related humans. The best way in which to begin to explore this possibility was through analyzing a sample of known individuals, with

known relationships to each other, that was known to be relatively self-contained in terms of marriage/breeding patterns. Knowledge of these factors makes the comparison of specimens within and between samples more informative. A well-preserved sample is also desirable in order to have the best chance to find unique features. The Spitalfields sample is the primary reference sample for this thesis because it fits the above criteria.

Even if each population is unique, it may not be possible to uncover characters that can demonstrate this uniqueness. One must start however, with the hypothesis that the skeletal sample of interest is unique, and therefore will exhibit unique morphological characters. Ideally, the formulation and testing of hypotheses of unique human groups would mirror the mechanics of systematic analyses. A familiar example can be taken from basic paleontological research. Generally, when paleontologists determine whether a specimen (or specimens) belongs to an already known species or subspecies, or whether the specimen belongs in a new group, they will compare the morphology of the specimen to the morphology of other, similar specimens. For paleoanthropologists, for instance, the specimen count for a given sample is often just a handful of or single skeletal element or fragment. These fragments can be compared to the totality of the available hominid fossil record with relative ease, given the availability of cranial casts and the extensive literature published (Schwartz and Tattersall, 2002; Schwartz and Tattersall, 2003; Schwartz and Tattersall, 2005).

The simplest way to test this hypothesis is to compare the sample of interest to other samples. In an ideal situation, an osteologist would be able to work in a similar fashion as a paleoanthropologist. Samples of human skeletal remains, whether found

in poor or good condition, often have a very large number of burials/skeletal elements to consider. This in itself makes the examination of multiple samples difficult in terms of time and effort. It is also impractical, if not impossible, to examine representative samples from populations all over the world. A relatively complete survey of nonmetric traits from skeletal samples across the world has been completed (Hanihara and Ishida, 2001a; Hanihara and Ishida, 2001b; Hanihara and Ishida, 2001c; Hanihara et al., 2003). This particular project, however, took many years and used characters commonly listed in skeletal analysis. To test hypotheses of the uniqueness of human groups would require novel examination of each, and continuing comparison. That is a goal for groups of researchers, perhaps through more than one generation.

Before one can begin to compare all samples, it is necessary to determine the viability of uncovering unique characters and delineating a single group. The Spitalfields sample will be used to answer this question.

If it is possible to find unique characters in different human groups, it should stand that these characters would also be unique not only to the particular group, but to humans in general. They would, therefore, not be found in any other type of hominoid. Non-human primate and extinct hominid forms, therefore, should be kept in mind when examining human skeletal morphology.

5.3.2 Spitalfields

The Spitalfields skeletal sample was recovered from the crypt of Christ Church with all Saints in the Spitalfields section of the City of London, England. The excavation of the crypt at the church proceeded from 1984 until 1986, as an extension of a restoration

project for the church which began in the 1970's. The first known burial was placed in the crypt at Christ Church in 1729, and the last in 1859 (Reeve and Adams, 1993). A total of 967 skeletons was recovered from the crypt, with 387 of the individual burials being of known sex and age at death because of coffin plaques and church mortuary records (Cox, 1996).

The Spitalfields skeletal sample has been examined in detail by other researchers, beginning with the official publications for the excavation project for the crypts of Christ Church (Molleson and Cox, 1993; Reeve and Adams, 1993). Such a large sample of human skeletal remains of known individual profiles presents a rare opportunity by which to gauge skeletal analysis against factual records of individuals at their times of death. The skeletal material is in generally excellent condition, providing an excellent opportunity for a complete examination of the skeletal elements critical for this study.

The skeletal sample from Spitalfields also represents a relatively closely linked community – Huguenot immigrants and their decedents, who perhaps, fled to England to escape religious persecution in France (Reeve and Adams, 1993). Of the named burials, approximately 41% were French, likely representing this Huguenot group, which over several generations eventually intermarried into the host population (Molleson and Cox, 1993). These Huguenot émigrés were best known as weavers, with their silk products representing some of the best luxury items available in the 17th and 18th century England (Cox, 1996; Reeve and Adams, 1993). As a result, many of the individuals represented in the Spitalfields were financially well-off, making the area around Spitalfields somewhat exclusive (Reeve and Adams, 1993). This wealth is also

reflected in the remains of the individuals, since many of the individuals had access to higher quality healthcare, which is demonstrated by those who had dental surgery. Many individuals in the Spitalfields sample are related, and the familial relationships written in the burial records (Appendix G).

The tightness of the community and known familial relationships of individuals make the Spitalfields skeletal collection make well-suited to test theories of using skeletal analysis to determine biological relationships between groups based on skeletal characters.

5.3.3 Terry Collection

The Terry Collection is a reference collection of skeletal material currently housed at the National Museum of Natural History, Smithsonian Institution in Washington, D.C. The collection was assembled from 1900 until 1941 by Robert J. Terry, the head of the anatomy department of Washington University in St. Louis. During his tenure, Terry collected a sample of documented skeletal specimens to which more skeletons were added until 1965 making a total of 1636 specimens (Stewart, 1979). The collection represents a cross-section of the early 20th century population of St. Louis. Its specimens are listed by ancestry (Black, White, or Asian), sex, and the age at death of the individual. The number and the excellent preservation of the specimens in the Terry Collection make them ideal for comparative study for morphological characteristics. This collection, therefore, has been used many times in important research, including studies that have developed methods for the determination of biological characters such as sex and age at death (Wienker, 1984).

There is a caveat, however, that such assumption of representativeness of a reference sample is very much population specific. Some populations are typically more robust or more gracile than others. The characters on which sex differences are based are different because of sexual dimorphism, and if different populations exhibit different appearances of robustness, then a direct comparison for the sex of specimens from different populations becomes problematic (Schwartz, 1995; Wienker, 1984).

Although the sample represents a narrow cross-section of a single area of the U.S., the preservation and documentation of the individuals make it a reasonable sample for comparison with the Spitalfields sample. And the broad nature of the Terry Collection sample in terms of sex, age, and ancestry should provide a good representation of human skeletal variation for the comparison.

The Terry Collection should be different enough from the Spitalfields collection, separated by enough time and distance that the two samples do not overlap as biological units. This difference in the samples also supports the Terry Collection as a good comparative unit for the Spitalfields collection.

5.3.4 Prehistoric North American Skeletal Sample 1 – The Campbell Farm Site

The collection of skeletal material excavated in Southwest Pennsylvania is currently housed in the Department of Anthropology, University of Pittsburgh. This collection derives from the excavations of the Campbell Farm site in Washington County, Pennsylvania, and represents a single occupation of Monongahela Indians. A total of 60 numbered of burials are in the collection. Although most specimens are quite fragmentary, many are preserved well enough to be used in the analysis.

5.3.5 Prehistoric North American Skeletal Sample 2 – The Perry Site

This collection of skeletal material is housed at the University of Alabama. The Perry Site, designated 1Lu25, is an archaic site located on Seven Mile Island in the Pickwick Basin of Alabama. The site was excavated in the 1930's as part of the WPA work relief programs that were responsible for so many excavations throughout the Southeast US during the Great Depression. There are a total of 141 burials from Unit One of the site (Newman and Snow, 1942). Most are in fair-to-good condition.

6.0 RESULTS

6.1 INTRODUCTION

The data collected using the methods outlined in Section 5.2 are presented in tabular form in Appendices A – D. This chapter, however, summarizes the specific skeletal traits used in the study and their appearance in specific samples, and if any could be considered unique to a given population.

The touchstone sample is the skeletal collection excavated from Christ Church at Spitalfields, London. Table 6.1 presents the nonmetric trait data from the published report on the anthropological examination of the excavated skeletal remains. None of the characters presented in the Spitalfields report (Molleson and Cox, 1993) is unique; they are listed in their frequency of appearance. Although there are traits that are expressed in very low frequency in the Spitalfields sample (e.g. the os japonicum) these traits are found in other skeletal samples from around the world (Hanihara et al., 2003; Hauser and De Stefano, 1989). By definition, therefore, none of these characters can be considered unique to the Spitalfields collection.

The traits listed in Table 6.1 are also listed in various bioarchaeological studies, (as discussed in Chapter 2) or can be found in various other texts that list different variable traits in human skeletal samples (Bass, 1987; Hauser and De Stefano, 1989; Schwartz, 1995). Because these traits are found in varying frequencies in multiple

Table 6.1: Nonmetric trait frequency from the official excavation research (after Molleson and Cox, 1993)

Trait	Frequency	%
Metopism	35/382	9.0
Hyoid	92/552	16.0
Hyoid Accessory	69/554	12.0
Inca ossicle	39/421	9.0
Lambdoid ossicle	145/427	34.0
Sagittal ossicle	13/446	3.0
Bregmatic ossicle	11/470	20.0
Coronal ossicle	56/471	120.0
Asterion ossicle	99/419	24.0
Parietal notch ossicle	113/426	27.0
Squamous-parietal ossicle	38/418	9.0
Epipteric bone	30/403	7.0
Os japonicum	1/381	.3
Highest nuchal line	200/443	45.0
Parietal foramen	329/485	68.0
Foramen of Huschke	12/581	2.0
Foramen ovale incomplete	4/412	1.0
Mastoid foramen exsutural	109/415	26.0
Post-condylar canal	277/436	64.0
Zygomatic foramen	242/452	53.0
Infraorbital foramen	330/386	85.0
Supraorbital foramen	60/400	15.0
Frontal foramen open	402/503	80.0
Anterior ethmoid foramen exsutural	117/381	30.0
Posterior ethmoid foramen exsutural	7/404	2.0
Accessory mental foramen	3/527	.6
Mandibular torus	14/400	305
Maxillary torus	71/464	15.0
Palatine torus	4/449	1.0
Frontal groove	71/793	14.0
Palatine bridge	12/464	3.0
Occipital condyle double	29/441	6.0
Occipital third facet	129/457	28.0
Precondylar tubercle	355/445	80.0
Fossa faringea	79/408	19.0

skeletal samples from around the world, they are not useful in a cladistic analysis that requires a morph to share unique anatomical traits.

Given the ideal of using a cladistic analysis the key, then, is to try to delineate a human skeletal sample, in this case the Spitalfields sample, as a genetically related group to be used in comparative studies. The cranial characters used in this study are described below, and the different coeds used in the scoring of the characters in the analyses. These codes are used in the appendices for ease of data recording and comparison.

6.2 METHOD OF EXAMINATION

The alpha taxonomy – the exploratory, descriptive phase (see Appendix F) – of the Spitalfields sample revealed possible unique skeletal traits and forms. The characters that appeared to form a pattern were coded according to their presence and form in a coding sheet (see Appendix A). The characters chosen for use in this study are meant to reflect developmental attributes. Ironically, the good preservation of the Spitalfields crania limited one aspect of the analysis. With the calvaria intact; characters within the skull could not be readily observed, and were not used in this project.

During the first examination of the Spitalfields collection, I determined that five general areas of the cranium should be examined for unique characters or unique forms of characters: the pterygobasal and orbital region, the zygomas, the basicranium, and the palate. These regions have also been the focus of numerous morphological studies due to their developmental and functional importance. Traits were recorded in this

study bilaterally where appropriate. Not all of the characters used were necessarily expected to be unique to the collection, but perhaps unique in their appearance. Therefore, some of the characters in the Spitalfields sample that stood out as possibly useful are some that have been described by other osteologists. The recording of characters that are not expected to be unique, such as the presence of a supraorbital foramen or notch, was not expected to yield information about a unique form as recorded, but to facilitate the possible observation of other unique characters in the same anatomical region during this analytical phase. Data from the complete analysis of the initial analysis of nonmetric traits of Spitalfields crania is presented in Appendix A.

The use of photographs was critical to the comparative analysis. The majority of the characters are illustrated in Figures 6.1 – 6.32. These photographs are not to scale. A list of the specimens and characters indicated in each figure is given in Table 6.2.

6.3 CRANIAL ANALYSIS

The description of the cranial analysis is broken into five sections for clarity – the pterygobasal region, cranial base, palate, orbital region, and the zygomas. Each trait has its own scoring indicators, but there are general scores used throughout the analysis for instances where the portion of the specimen analyzed is present but too damaged for analysis, if the portion is absent, or if the character is obscured or indeterminate for another reason.

DAM = Damage

- = Absent/Not available

+ = Superlative, when present with other codes

? = Indeterminate

V = Very

6.3.1 Pterygobasal region

The base of the skull, the inferior aspect of the greater wing of the sphenoid, and the petrous portion of the temporal bone in particular, have been the focus for studies on human evolution and variation. For instance, as Braga et al. (1998) demonstrate, the differential appearance of the foramen ovale and foramen spinosum can illuminate evolutionary differences in extant apes, fossil hominids and humans. Given the complex nature of the development of the cranium, specifically in regard to the formation of the pattern of the bone relative to the neurovascular structures, as well as the functional aspect of the cranium and its position in regard to walking bipedally or quadrupedally (knucklewalking, etc.), this anatomical region could potentially contain characters that could distinguish between human groups. It is also true for the region of the basicranium (see below).

6.3.1.1 Lateral pterygoid plate/ptergospinous bridging

The lateral pterygoid plate was scored for breadth and whether it extended beyond and over the foramen ovale and foramen spinosum (Figures 6.1 through 6.12). If a bridge is present, the medial pterygoid nerve and a branch of the maxillary artery usually traverse the pterygospinous foramen (Hauser and De Stefano, 1989). Specific forms of bridging were noted and photographed. Partial bridging was also recorded, as

this is the same phenomenon as bridging. Width was scored as wide if any portion of the posterior margin of the lateral pterygoid plate reached posteriorly as far as the foramen ovale in the coronal plane. A score of “very wide” indicates the extension of the lateral pterygoid plate beyond the anterior most border of the foramen ovale. Otherwise the width of the lateral pterygoid plate was recorded as “normal.” A wide lateral pterygoid plate does not necessarily indicate the presence of bridging. The presence of any bridging was scored in the same cell as the width of the lateral pterygoid plate, and either as present or as absent. Although the same hyperostotic phenomenon, partial bridging was indicated in the Notes section of the scoring tables.

W = Wide
VW = Very wide
N = Normal
+ = Bridging present
0 = Bridging absent

6.3.1.2 Foramen ovale and foramen spinosum

Given the importance in development of the foramen ovale (which transmits the mandibular nerve and the accessory meningeal artery) and of the foramen spinosum (which transmits the middle meningeal artery and the meningeal branch of the mandibular nerve) the shape and size of the foramen ovale and the size of the foramen spinosum were recorded. Any differences from the expected position of both foramina were also noted; if the foramen spinosum was in the point of the spine, or if either foramen opened into the fissure, for instance. Unusual bony growth was also noted, as in a bony loop that has formed over the foramen spinosum (Figure 6.13), or bridge (Figure 6.14). The shape of the ovale was scored as “oval” if one axis was obviously

longer than the other; “round” if it was close to being circular. Size was judged relative to the width of the pterygoid spine. If the foramen ovale or spinosum visually covered 50% or less of their area of their portion of the pterygoid spine, they were recorded as small. If the area was 75% or greater, they were recorded as large. Any area size in between was recorded as moderate.

L = Large O = Oval
M = Moderate R = Round
L = Large

6.3.1.3 Foramen lacerum

In life, the foramen lacerum is not a foramen at all, but is filled with cartilage, which represents the incomplete ossification of the petrous portion of the temporal bone. While no vessels or nerves course through the foramen lacerum, with the occasional exception of an emissary vein, the degree to which the petrosal is ossified may demonstrate a pattern in a skeletal sample (Figure 6.15). The size was gauged as “small” if the foramen was close to complete closure with the basicranium; “normal” (here, meaning moderate) if the patency appeared to be 5-25%; and “large” if there was significant incomplete ossification, representing more than approximately 25% of the medial portion of the petrous portion of the temporal bone.

L = Large
M = Moderate/normal
S = Small

6.3.2 Cranial Base

6.3.2.1 Basion

Several specimens in the Spitalfields collection exhibited a small bony growth at basion. The observed "spur" appears to be syndesmotic, and in some cases projects into (Figure 6.16) or inferiorly away from the base of the skull (Figure 6.17). The presence or absence of any growth at basion was recorded, including bony bumps that were paired at the anterior border of the foramen magnum (called precondylar or basilar tubercles). This particular trait manifestation may represent the insertion points for the rectus capitis anterior muscles or for the ligaments that join the basiocciput and the first two cervical vertebrae (Hauser and De Stefano, 1989). These tubercles (Figure 6.18) are unlike the bony projection located at basion. Differences in the appearance of the character were recorded in the Notes section of the scoring forms.

\+ = Presence of the spur

0 = Absence

6.3.2.2 Jugular processes

The presence or absence of a rough bony growth on the jugular processes, lateral to the foramen magnum, was observed on several specimens and. The amount of growth was recorded as well (either a moderate amount or a great deal of growth was noted) (Figure 6.19 – 1). This character is not the same as the paracondylar process (Hauser and De Stefano, 1989), as it is generally less dramatic in appearance and more laterally placed.

0 = None

S = Small

M = Moderate

L = Large

6.3.2.3 Jugular foramen

Bridging of the jugular foramen was noted. In this specific case the bridging divides the foramen (Figure 6.19 – 2). The bridge, which most likely represents the ossification of fascia that separates the internal jugular vein, the internal carotid artery, the vagus nerve, or the glossopharygeal nerve, or the product of the ossification of cartilaginous processes that appear in development (Hauser and De Stefano, 1989). In either case, this character appears early in development.

\+ = Present

0 = Absent

6.3.2.4 Postglenoid plate

During the first pass of the examination of the Spitalfields sample, some of the specimens appear to have noticeably larger postglenoid plates (of the temporal bone), with striations running superioinferiorly (Figure 6.20). The postglenoid plate was scored for normal appearance, or large with the striations.

S = Small

M = Medium

L = Large

6.3.2.5 Vomer relative to spheno-occipital synchondrosis

The position of the alae of the vomer relative to the synchondrosis was recorded, whether the alae of the vomer are level with (Figure 6.21), or anterior (Figure 6.22) or posterior (Figure 6.23) to the synchondrosis. The position of any landmark on the

basicranium relative to the spheno-occipital synchondrosis is likely a function of the skull being positioned directly on top of the spinal column as part of the evolved ability to walk bipedally.

Even = Even with the synchondrosis

Behind = Posterior border of the vomer is anterior to the synchondrosis

Beyond = Posterior border of the vomer is posterior to the synchondrosis

J = Just (as in just beyond, just behind)

6.3.3 Palate

6.3.3.1 Bony spurs/ridge

The presence of significant bony growth on the hard palate related to the path of the greater palatine nerves and blood vessels was recorded (Figure 6.24). Any spur-like growth was scored, as was the presence of a slight ridge coursing between the greater and lesser palatine foramina (Figure 6.25 – 1).

\+ = Present

S = Slight/small

0 = Not present

6.3.3.2 Greater palatine foramen

The general depth (deep or shallow) and shape (oval, round or slit-like) of the palatine foramen was recorded (Figures 6.25 – 2 and 6.26). The greater palatine foramen communicates the greater palatine nerve as it descends from the pterygopalatine ganglion. Shape is recorded first, then depth.

S = Slit-like D = Deep

O = Oval
S = Shallow
R = Round

6.3.3.3 Palatal shape

The general shape of the posterior border of the horizontal plate of the palatal bones, as they appear articulated in situ, was recorded. The general anterio-posterior width of the lateral plate of the palate was recorded as either “narrow,” “normal,” or “wide.” The width was generally scored as “normal,” with “wide” and “narrow” being scored only in cases where the width was obviously much narrower or wider than to be expected. The coding for the shape of the palate bone is a combination of the relative anterior-posterior width of the palate bone, and the general shape of the posterior border of the palate/posterior nasal spine. In some of the coding the full code word is typed. For instance, as seen in Figure 6.27, specimen 2178 was coded as moderate and blunt (MODBLUNT), and in Figure 6.28, specimen 2812 was coded as moderate and slightly blunt (MODSLBLUNT).

THIN = Thin
FL = Flat
MOD = Moderate width
SQ = Square
THICK = Thick/wide
PT = Point
SL = Slight
BL = Blunt

6.3.4 Orbit region

While not as complex in development or in morphology as the basicranium, the bony structures of the face are easily accessible, and the upper portion of the splanchocranium often preserves better in the archaeological record than the lower portion; this includes the zygomatic region (discussed below).

6.3.4.1 Supraorbital foramen/notch

The presence of either a supra orbital foramen or notch, or both, and in what number they appeared, was recorded. These alternate forms of expression of the same trait are often recorded in nonmetric studies. The presence of a canal or the presence of a notch likely have different genetic etiologies (Hauser and De Stefano, 1989). The different appearances of the morphologies of the bone could, therefore, indicate different morphologies of the blood vessels and nerves. The different morphologies of the bone likely indicate differences in the genetic instruction that controls the branching morphogenesis of the nerves and blood vessels during development.

N = Notch
F = Foramen
B = Both

6.3.4.2 Infraorbital foramen

Two basic features of the appearance of the infraorbital foramen were noted. First, the appearance of a “lip” that partially covers the foramen was recorded for its presence or absence. The presence of this character gives the foramen an almost crescent moon form. The second character recorded for the infraorbital foramen was the direction in which it opens, generally medially, inferiorly, or a combination of the two directions (Figure 6.29). The presence of a lip also often corresponded with a robust appearance of the infraorbital margin.

A single infraorbital foramen typically communicated a single infraorbital neurovascular bundle. The appearance of multiple infraorbital foramina also may indicate differences in the genetic instruction of the branching pattern of the infraorbital blood vessels and nerve. Just as with the supraorbital neurovasuclature, differences in

the genetic instruction for the branching morphogenesis of the neurovascular structures found below the orbit may yield distinctive morphology.

L =Lip
0 = No apparent lip
I = Inferior
M = Medial

6.3.4.3 Infraorbital margin

The shape of the infraorbital margin was recorded. Specifically, many of the Spitalfields specimens were noted in the initial observation as having a "rolled" appearance (Figure 6.30), i.e. margin is blunt and rounded. This is in contrast to a sharp, edge-like appearance of the infraorbital margin. The rolled infraorbital margins are often also robust in appearance.

0 = Normal
+ = Rolled
V = To a large degree

6.3.4.4 Infraorbital margin angle

The mediolateral angle of the inferior portion of the orbit rim was recorded. The angles were scored as angled (approximately 45 degrees, Figure 6.31 – 2), slightly angled (approximately 25 to 40 degrees, Figure 6.32 – 2) and level (under 20 degrees).

A = Angled
SA = Slightly angled
L = Level

6.3.4.5 Trochlear spur

The presence or absence of the trochlear spur in the orbits was recorded. A trochlear spur is a hyperostotic feature that represents the ossification of the connective tissue loop (the trochlea) through which the tendon of the trochlea muscle courses aiding in its function in eye movement. There is debate about the timing of the appearance of the spur, whether it appears early in life or later (Hauser and De Stefano, 1989).

+ = Present
0 = Absent

6.3.5 Zygomas

6.3.5.1 Zygomatic tubercle

The zygomatic tubercle occurs in the region of the zygomatic arch that generally marks the most inferiomedial aspect of the bone, lateral to the inferior end of the zygomaticomaxillary suture. It is also part of the origin for the masseter muscle, and thus appears more robust that the rest of the zygomatic bone. The position of the tubercle, relative to the Frankfurt horizontal plane, was scored as whether "above" (Figure 6.30 – 1), "level," or "below" (Figures 6.31 – 1). The presence of one protuberance (normal) or two protuberances (double).

L = Level
B = Below
U = Above
N = Normal
D = Double

6.3.5.2 Zygomaticomaxillary suture

The course of the zygomaticomaxillary suture was drawn to determine unique patterns (see Appendix A).

Any appearance of a character, listed above or not, that is of unusual appearance was briefly described in the “Notes” column of the data sheets.

Table 6.2: Spitalfields specimens illustrating recorded nonmetric characters

Figure	Specimen	Character
6.1	2720	Pterygospinous bridging, with a “clover-leaf” appearance to the foramen (full shot)
6.2	2720	Pterygospinous bridging, with a “clover-leaf” appearance to the foramen (close-up)
6.3	2918	Pterygospinous bridging
6.4	2908	Incomplete pterygospinous bridging
6.5	2872	Pterygospinous bridging
6.6	2186	Pterygospinous bridging with suture-like structure in the middle (full shot)
6.7	2186	Pterygospinous bridging with suture-like structure in the middle (close-up)
6.8	2189	Pterygospinous bridging with suture-like structure in the middle
6.9	2369	Pterygospinous bridging obscured by desiccated soft tissue
6.10	2464	Pterygospinous bridging over the foramen ovale only; bony spur positioned lateral to the ovale
6.11	2498	Pterygospinous bridging creating separate bridges over the foramen ovale and the foramen spinosum
6.12	2173	Pterygospinous bridging with suture-like structure in the middle
6.13	2169	Curved loop of bone over the foramen spinosum
6.14	2184	Bony bridge over the foramen spinosum
6.15	2178	Moderate patency of the foramen lacerum
6.16	2251	Unusual bony spur at the midline of the anterior border of the foramen magnum
6.17	2173	Unusual bony spur at the midline of the anterior border of the foramen magnum
6.18	2185	Tubercles likely the insertion points for the rectus capitis anterior muscles
6.19 – 1	2231	Roughened surface of the jugular process
6.19 – 2	2231	Bifurcation of the jugular foramen
6.20	2872	Large postglenoid plate with striations
6.21	2178	Position of the alae of the vomer are even with to the spheno-occipital synchondrosis
6.22	2507	Position of the alae of the vomer are anterior to the spheno-occipital synchondrosis
6.23	2515	Position of the alae of the vomer reach posterior to the spheno-occipital synchondrosis
6.24	2917	Bony spurs on the lateral side of the hard palate (maxilla)
6.25 – 1	2187	Ridge coursing between the greater and lesser palatine

Figure	Specimen	Character
		foramina
6.25 – 2	2187	Greater palatine foramen described as round and deep
6.26	2575	Greater palatine foramen described as slit-like and shallow
6.27	2178	Thick/broad width of the palate bone, with blunt posterior nasal spine
6.28	2812	Moderate width of the palate bone, with slighlt/blust posterior nasal spine
6.29	2142	Infraorbital foramen lip, and inferiomedial angle of opening
6.30	2169	Rolling of the infraorbital margin
6.31 – 1	2556	Inferior zygomatic border dips inferiorly on the Frankfurt horizontal
6.31 – 2	2556	Distinct angle of the inferior orbital margin
6.32 – 1	2634	Inferior zygomatic border angles superiorly to the Frankfurt horizontal
6.32 – 2	2634	Slight angle of the inferior orbital margin

Figure 6.1: Spitalfields specimen 2720

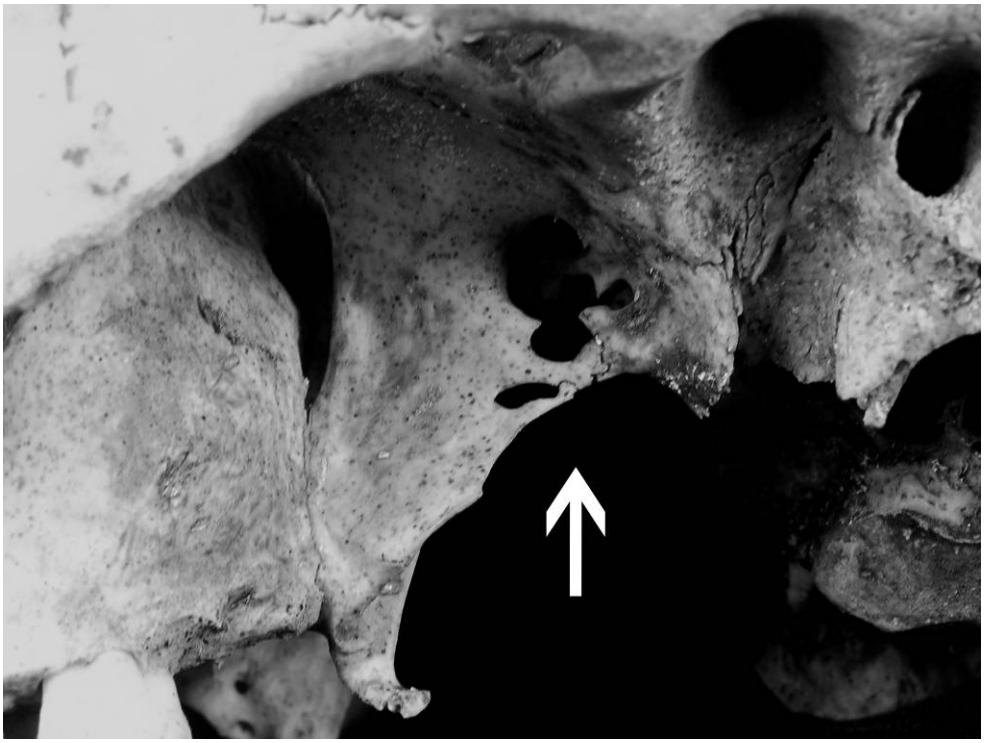


Figure 6.2: Spitalfields specimen 2720, left side close-up

Figure 6.3: Spitalfields specimen 2918

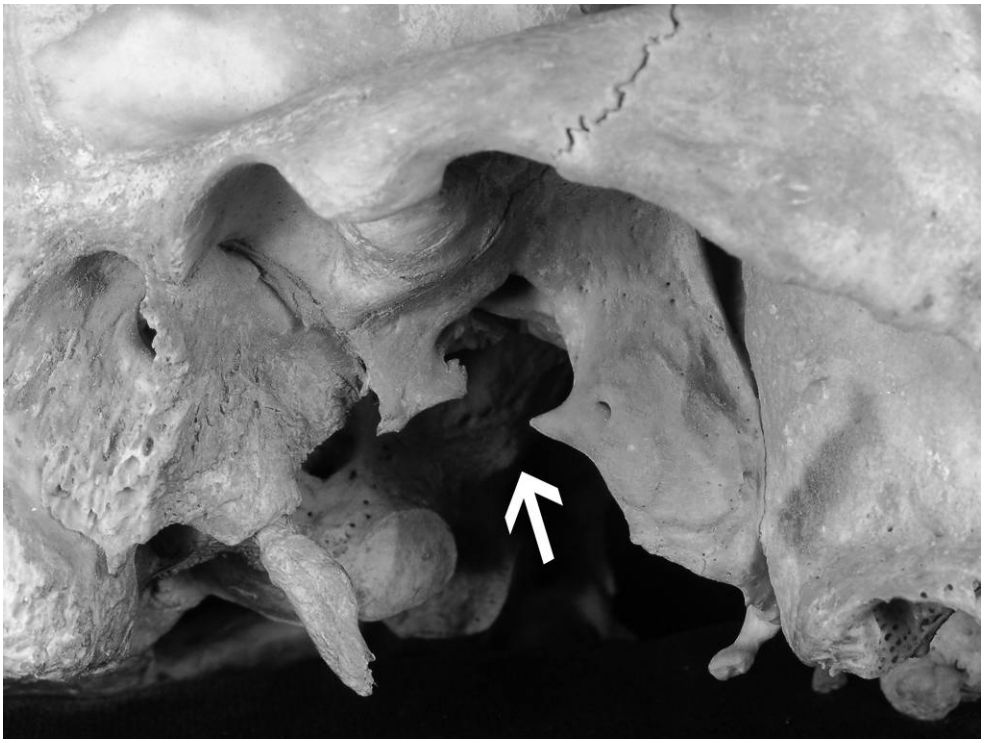


Figure 6.4: Spitalfields specimen 2908

Figure 6.5: Spitalfields specimen 2872

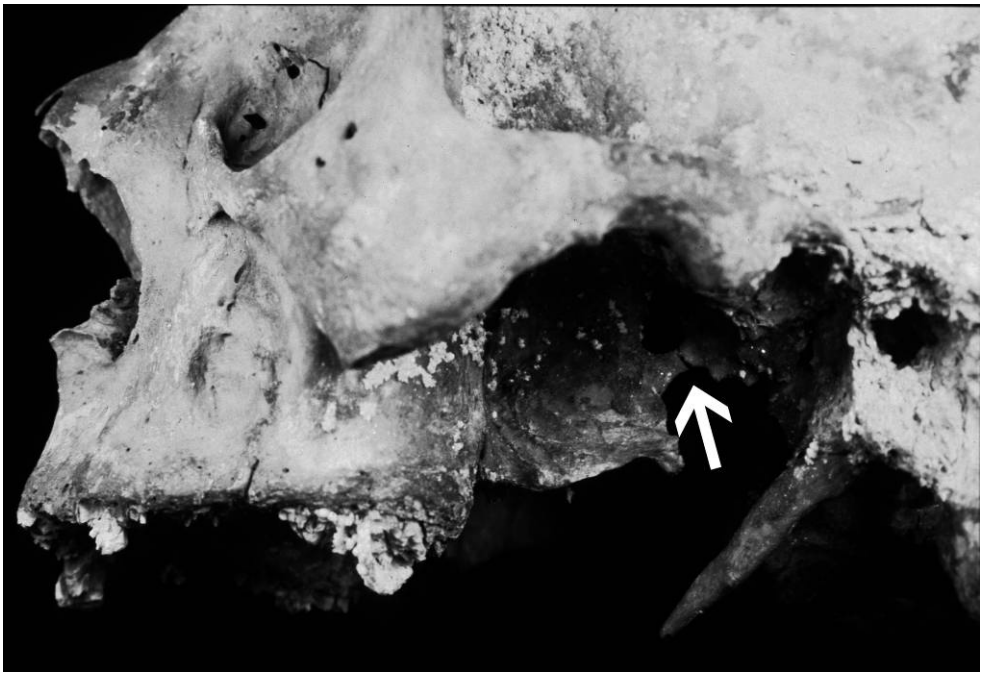


Figure 6.6: Spitalfields specimen 2186

Figure 6.7: Spitalfields specimen 2186

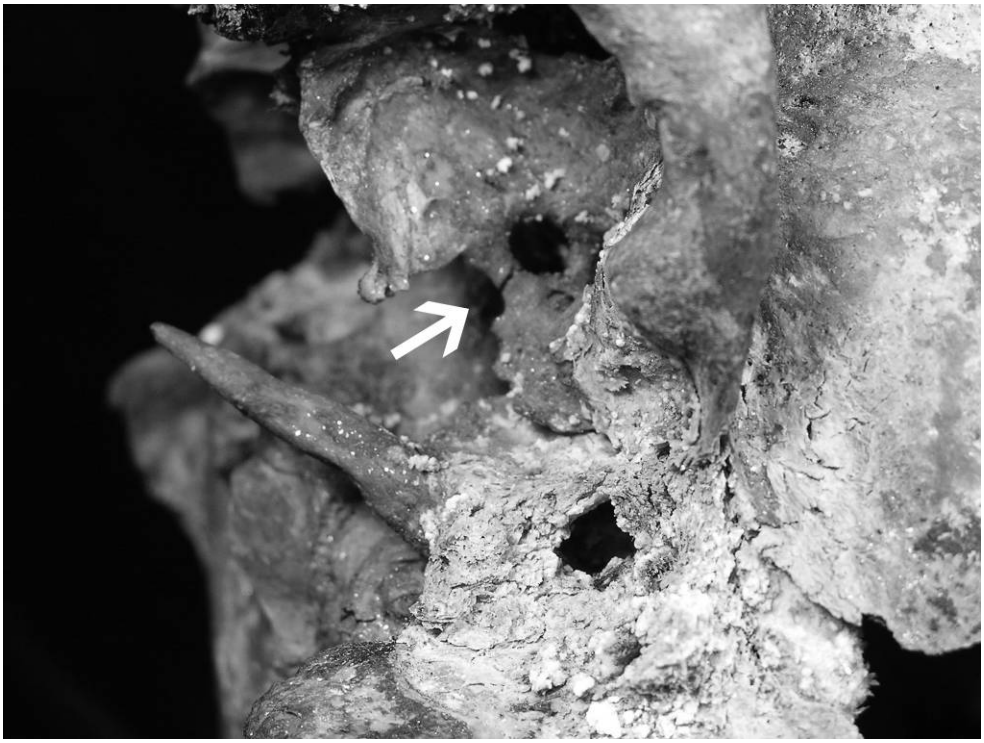


Figure 6.8: Spitalfields specimen 2189

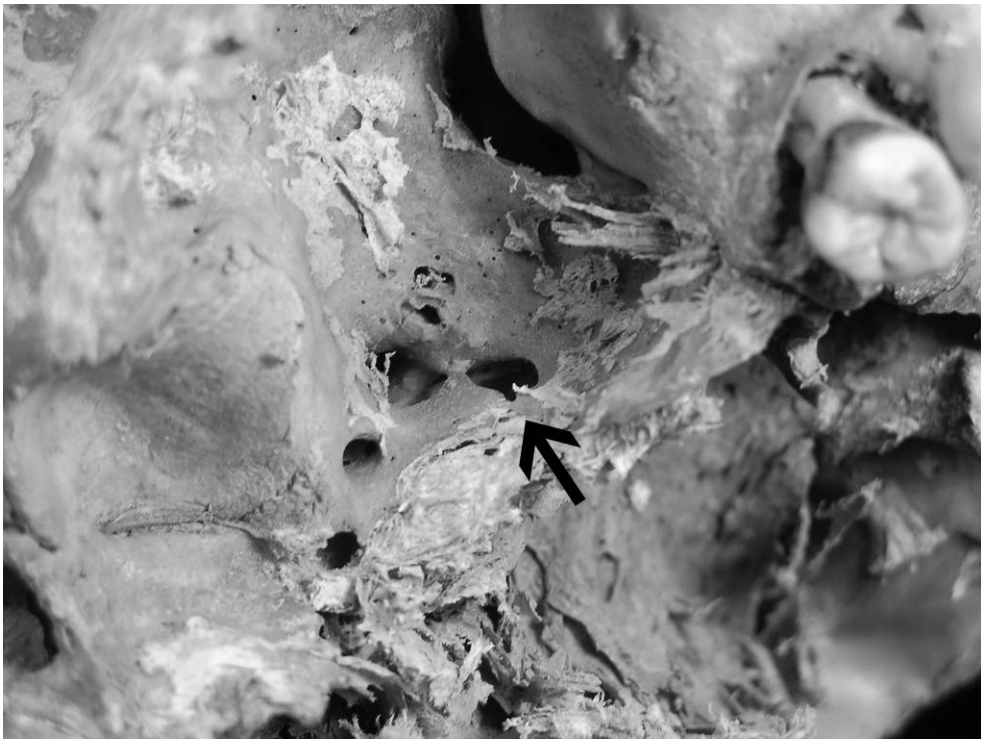


Figure 6.9: Spitalfields specimen 2369

Figure 6.10: Spitalfields specimen 2464

Figure 6.11: Spitalfields specimen 2498

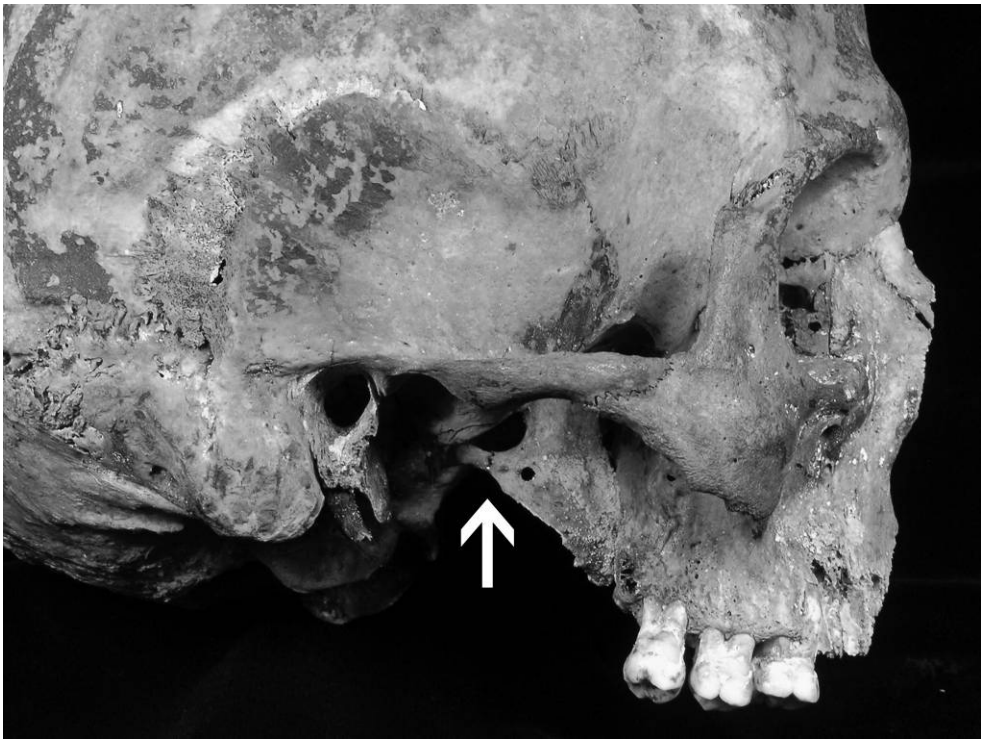


Figure 6.12: Spitalfields specimen 2173

Figure 6.13: Spitalfields specimen 2169

Figure 6.14: Spitalfields specimen 2184

Figure 6.15: Spitalfields specimen 2178

Figure 6.16: Spitalfields specimen 2251

Figure 6.17: Spitalfields specimen 2173

Figure 6.18: Spitalfields specimen 2185

Figure 6.19: Spitalfields specimen 2231

Figure 6.20: Spitalfields specimen 2872

Figure 6.21: Spitalfields specimen 2178

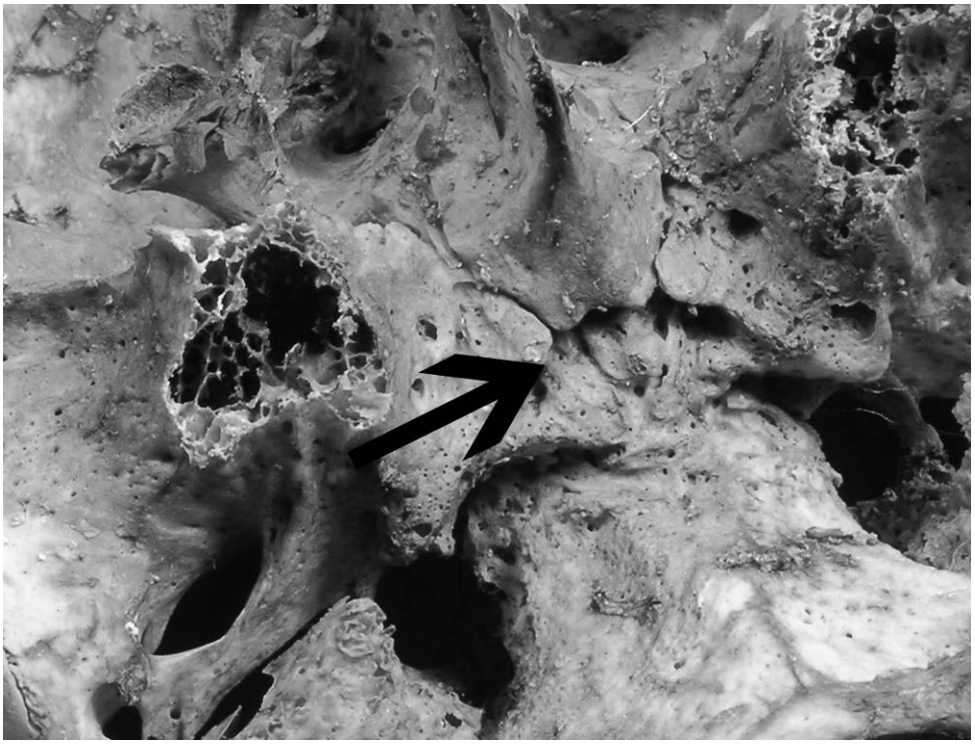


Figure 6.22: Spitalfields specimen 2507

Figure 6.23: Spitalfields specimen 2515

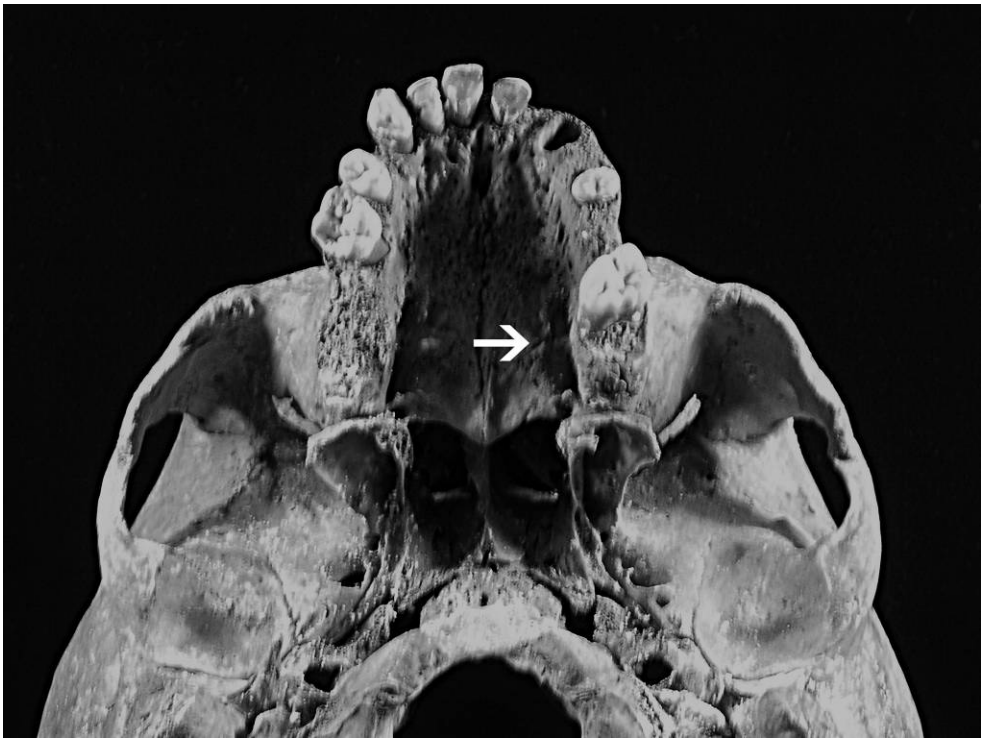


Figure 6.24: Spitalfields specimen 2917

Figure 6.25: Spitalfields specimen 2187

Figure 6.26: Spitalfields specimen 2575

Figure 6.27: Spitalfields specimen 2178

Figure 6.28: Spitalfields specimen 2812

Figure 6.29: Spitalfields specimen 2142

Figure 6.30: Spitalfields specimen 2169

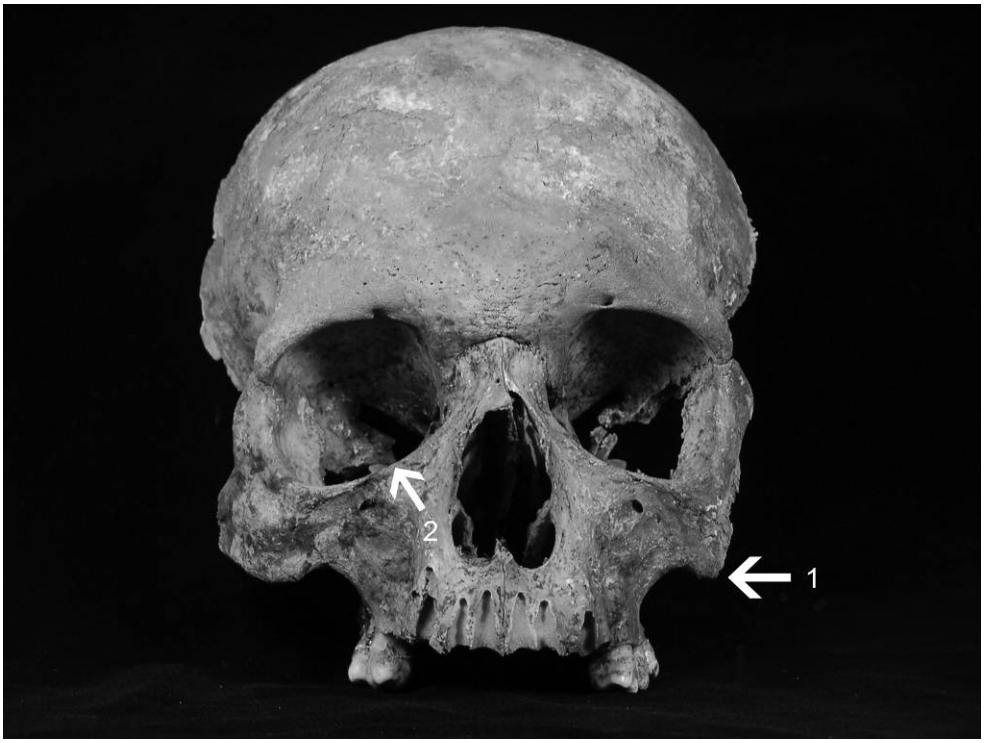


Figure 6.31: Spitalfields specimen 2556

Figure 6.32: Spitalfields specimen 2634

Many of the characters that were used to explore the possibility of the presence of a unique trait in the Spitalfields sample are hyperostotic (e.g. pterygospinbous bridging). This may be due to one of two things. Either these traits are easier to spot, or for whatever reason the Spitalfields sample, genuinely displays more hyperostotic characters. One unusual, but not unique, hyperostotic trait that appears in many of the individuals of the Spitalfields sample is ossified thyroid cartilage (Appendix A – Notes). Ossified thyroid cartilage, at least partially, was found in 37 individuals. The ossification of the thyroid cartilage begins just after the end of adolescence, and continues through life (Kirsch and Claassen, 2000). Regulated, in part, by vascular endolethial growth factor (VEGF) and its receptors, the ossification of articular cartilage, such as the thyroid cartilage, is relatively uncommon (Kirsch and Claassen, 2000; Pufe et al., 2004). There is the possibility that the appearance of this trait is due to a metabolic difference in a family group, but only one family group of named individuals ("Gamage" – Appendix G) has more than one individual with ossified thyroid cartilage.

Many of the characters in the analysis did not form any pattern at all. Palate shapes were almost all different in one way or another. This is also true of the configuration of the zygomatico-maxillary sutures. These characters are used in the analysis of the comparative samples, but in the final analysis are not given as much consideration as other characters.

6.4 COMPARISONS AND RESULTS

6.4.1 Preservation Differences in the Samples

The difference in preservation of the skeletons in the samples did affect how much can be accomplished in a comparative analysis. The Spitalfields collection, as a historical resource recovered from crypt burials that were relatively well-protected, is in excellent condition, especially for an archaeologically recovered sample that has been used many times for different individual's osteological research. The Terry Collection, which was collected from cadavers, is in almost perfect condition even after handling by hundreds of researchers. These two collections are in exceptional condition when compared to most collections, specifically archaeologically recovered skeletal material.

The archaeological samples are more representative of the state of preservation with which osteologists usually must contend. These collections are in good condition, but also show the limitations of comparing less-than-perfect specimens. A limited number of elements have the portions with the characters used in a comparative study. Good preservation can, however, have its drawbacks. The crania of the Spitalfields Collection, for instance, do not have the calvaria removed making it impractical to observe any characters viewable from inside the braincase.

6.4.2 Cranial character comparison results

Almost none of the characters identified in this analysis was revealed as unique to the Spitalfields sample. Hyperostotic characters dominated the analysis of the crania, in part because of their obvious appearance in the Spitalfields collection. Traits such as

pterygospinous bridging or bridging of the jugular foramen are by no means unique. In general, characters typically were either of consistent form or rare and of varying appearance. A comparison of characters in Appendix E (minus the complex characters that did not show a pattern, such as the shape of the palate) shows the percentages of characters appearing in each sample showing almost all that the cranial characters used in the analysis are found in all of the samples tested.

Only one character – the small bony projection that appears at basion – was present in the Spitalfields collection and not in any of the other samples. This character appears in Specimens 2251 and 2278. This spur is not related to the insertion points for the rectus capitis muscles, which generally appear as two bilateral elevations just anterior to the foramen magnum. This spur that appears in the Spitalfields specimens appears to not be described in any of the relevant literature either. Even if this character is unique, it would be the only one that, within the current analysis, would be a unique indicator of the population. However, one cranial character, and in so few individuals, is insufficient to distinguish the population.

6.4.3 Terry Collection

Characters that appear in the Terry Collection, or any other sample, cannot be considered unique for another sample or apparent group. This means that the raits that may have delineated the Spitalfields sample and appear in the Terry Collection or other samples provide a rejection of the hypothesis that the character states delineate that particular group. For instance, similar forms of pterygospinous bridging that were observed in the Spitalfields collection are present on specimens in the Terry collection

(Figures 6.33 and 6.34), including the “cloverleaf” pattern of the foramen (Figure 6.34 – 1). Figure 6.34 also shows a large postglenoid plate with striations.

Other traits found in the Spitalfields sample are readily observed in specimens from the Terry Collection. For example, Figure 6.35 (1) shows the lip and inferiomedial course of the infraorbital foramen, and (2) shows the “rolled” appearance to the infraorbital area. Figure 6.36 (1) demonstrates the presence of the palatal spurs and (2) the ridge of bone between the greater and lesser palatine foramina. Figure 6.37 (1) shows the palatal shape and (2) the position of the alae of the vomer to the spheno-occipital synchondrosis.

Figure 6.33: Terry Collection specimen 880

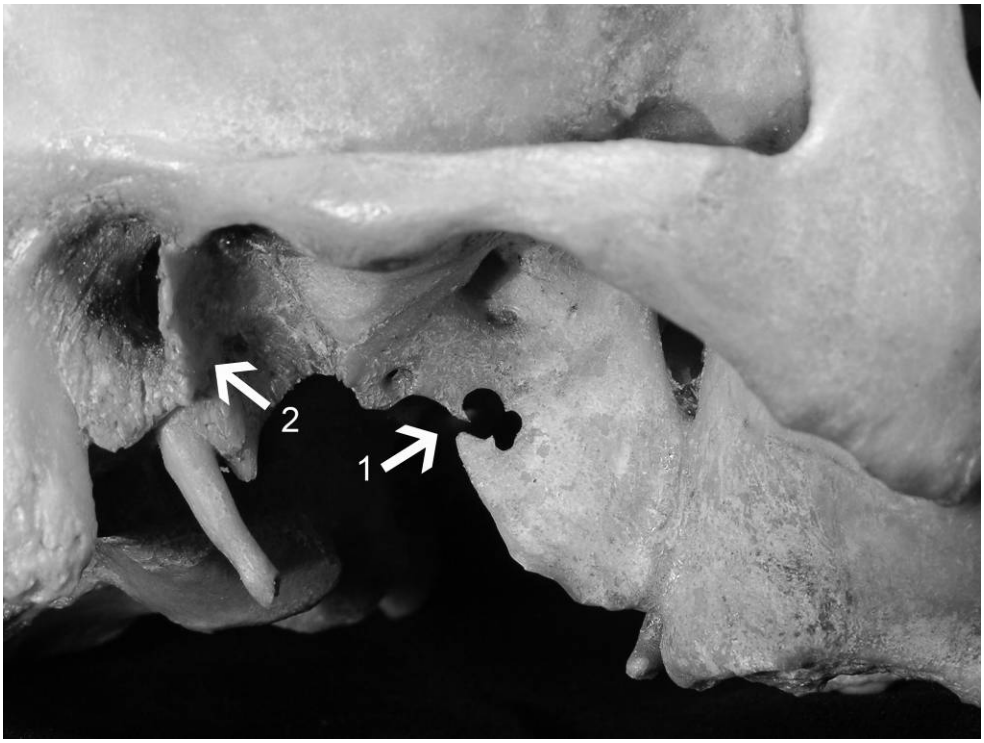


Figure 6.34: Terry Collection specimen 928

Figure 6.35: Terry Collection specimen 763

Figure 6.36: Terry Collection specimen 913

Figure 6.37: Terry Collection specimen 933R

6.4.4 Archaeological Samples

Since skeletal material recovered from the archaeological record is commonplace, specimens thus acquired form the basis of biodistance analsyis. Of primary importance when approaching archaeologically-derived samples is the issue of preservation vs. diagenetic processes. Poorly preserved remains provide little or no opportunity to elucidate biological/genetic relationships, much less the basic profile characteristics, such as sex and age.

Although the samples from the Perry Site and from Campbell's Farm are in reasonably good shape, the preservation is such that it is not possible to an even comparison for all characters used in this study. This problem is specifically addressed after the comparison of the results of the data for all of the samples.

6.4.5 Monongahela (Campbell's Farm) Collection

The Monongahela skeletal sample is in fairly good condition, although none of the individual skeletons is complete. Many elements have been damaged through diagenetic processes prior to excavation, and by storage and handling after excavation. Some of the skeletal material has been reconstructed (e.g. Figure 6.42). In spite of these problems, enough skeletal elements were in sufficiently preserved to yield some comparative nonmetric data (Appendix C). There are, however, lacunae in the data that makes comparison between samples difficult. The sample presents characters that had initially been delineated as potentially unique to the Spitalfields sample, like the Terry

Collection sample. The sex and general age were determined by the author and are presented in Appendix C.

Several characters are presented in the figures below (Figures 6.38-6.45) to demonstrate the presence of characters that are also present in the other samples. First, note the difference in preservation with this archaeological sample and the historical samples of Spitalfields and the Terry Collection (e.g. Figures 6.38 and 6.41). The crania in the figures below represent some of those that are in the best condition in. Forms of pterygospinous bridging is present in the Campbell Farm sample as in the others (Figures 6.38, 6.39, 6.42, and 6.43). Figure 6.40 shows a good example of an infraorbital margin with a rolled appearance. Figure 6.44 demonstrates three characters in the analysis: (1) the greater palatine foramen which is scored as oval and deep, (2) the bony ridge between the lesser and greater palatine foramina, and (3) the right jugular foramen is bridged. As a final example, Figure 6.45 shows the bony spurs present on the palatal portion of the maxilla. Also of general interest, but not for comparative purposes here, are the presence of foramina of Huschke bilaterally in Burial 69 (Figure 6.41).

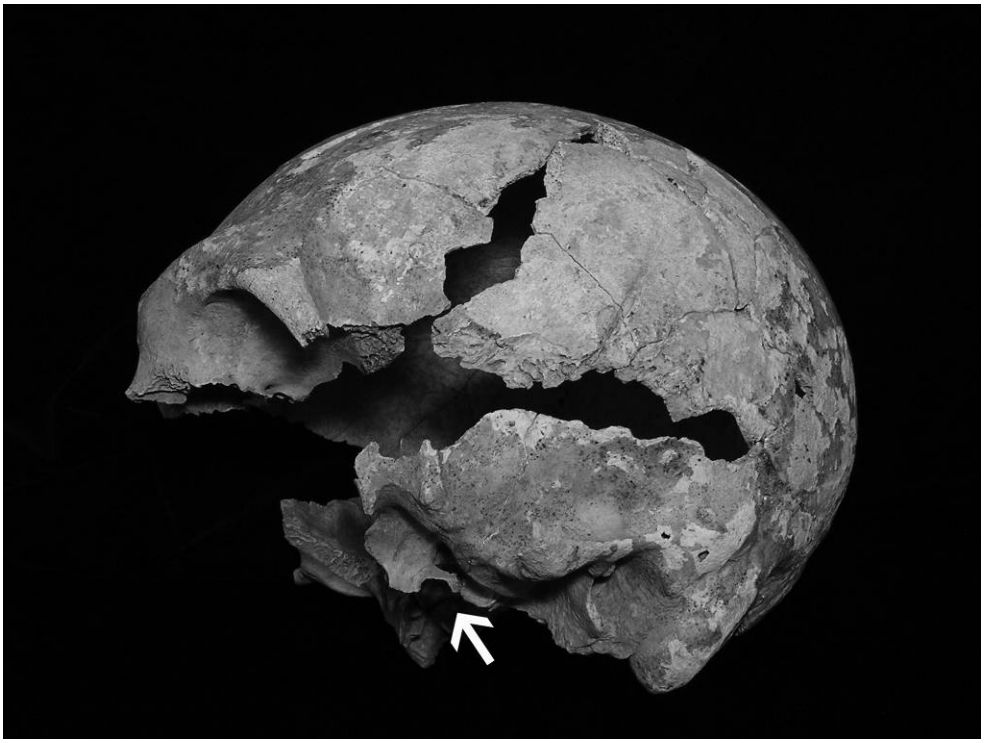


Figure 6.38: Campbell's Farm Burial 6

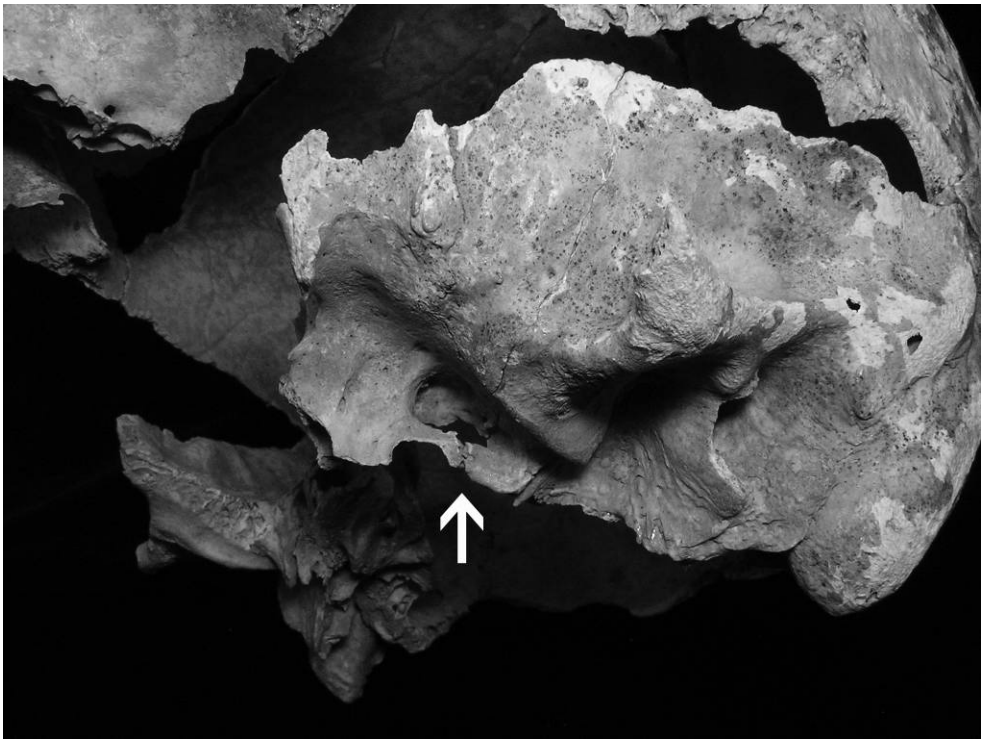


Figure 6.39: Campbell's Farm Burial 6

Figure 6.40: Campbell's Farm Burial 69

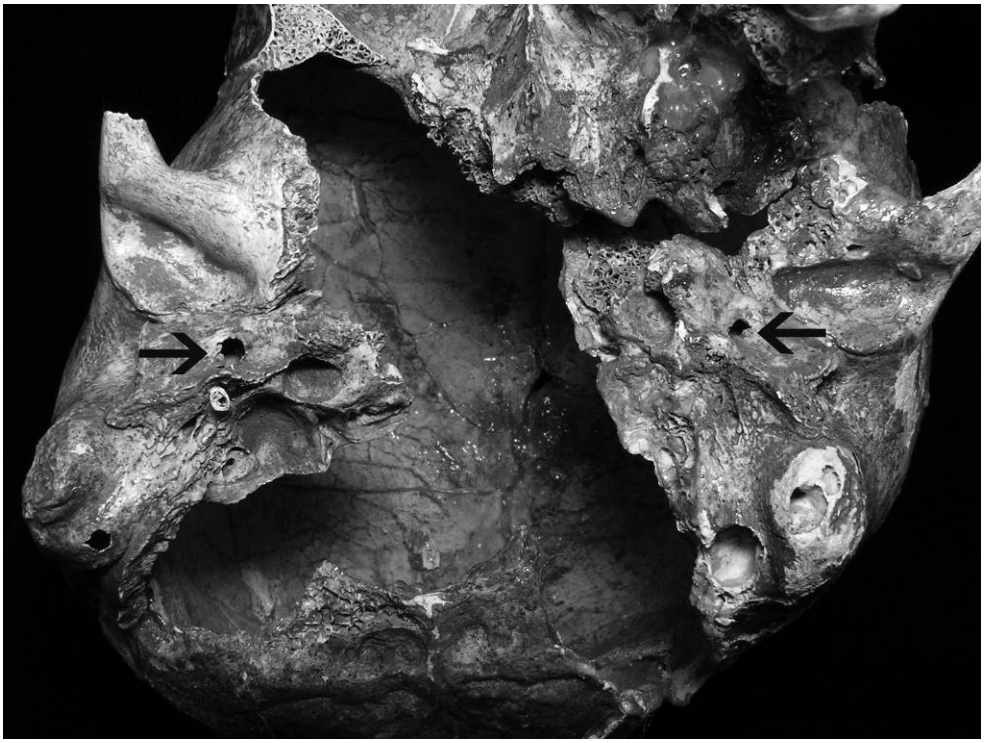


Figure 6.41: Campbell's Farm Burial 69

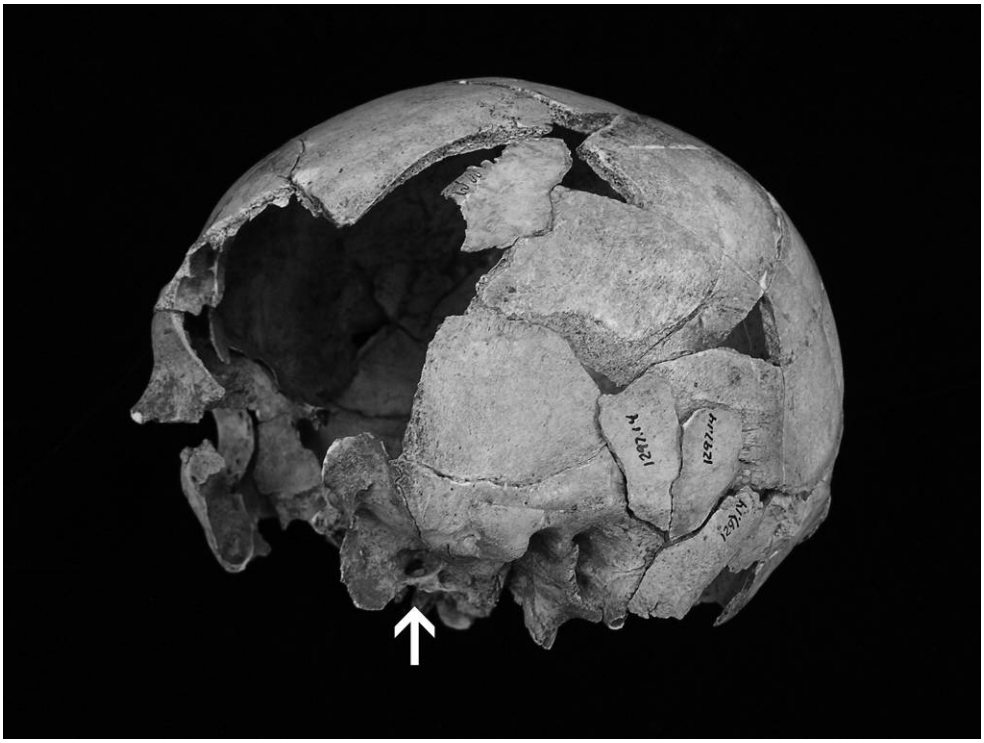


Figure 6.42: Campbell's Farm Burial 62

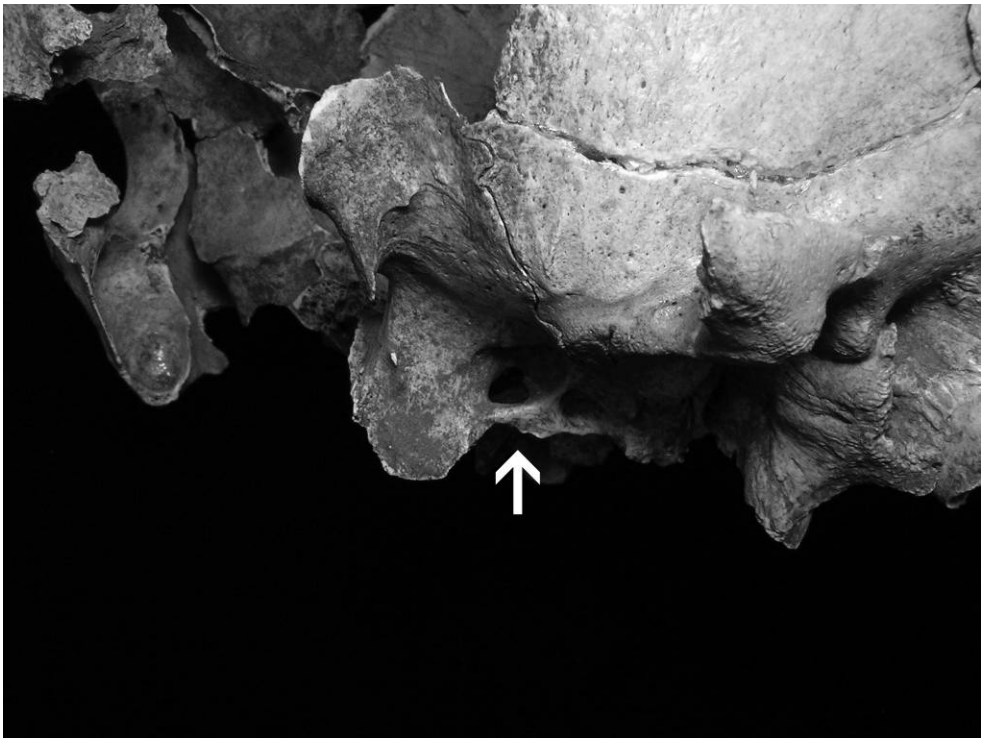


Figure 6.43: Campbell's Farm Burial 62

Figure 6.44: Campbell's Farm Burial 47

Figure 6.45: Campbell's Farm Burial 5

6.4.6 The Perry Site

Because the condition of the skeletal remains from the Perry Site is very good, especially when the antiquity of the material is considered, a few of the crania have been reconstructed (see Figures 6.49 and 6.52). The crania seem to have been reconstructed during around 70 years ago. None of the burials have been analyzed except for basic characteristics such as sex and general age (Keith Jacobi, personal communication). These data, which were gleaned form records on file at the University of Alabama, for age and sex are presented in Appendix D. Also presented in Appendix D are the raw data of recorded characters. As with the Campbell's Farm collection, the condition of the material limited the comparative analysis. Also, as with the Terry Collection, the large amount of material required that a subsample of the burials was used. A total of 61 crania were examined.

The state of preservation can be seen in the figures below (Figures 6.46 – 6.53). Reconstruction can be seen in Burial 296, with the mandible glued on (Figures 6.49 and 6.52). The worst preservation is associated with the absence and extensive damage to the lower splanchnocranium (Figures 6.48 and 6.51). The anterior view of Burial 220 (Figure 6.46) shows (1) the significant angle of the medial infraorbital margin, (2) the rolled appearance of the infraorbital margin, and (3) the lip of and mostly inferior course of the infraorbtial foramen. Figure 6.46 shows a, inferomedial course of the infraorbital foramen and an inferior border of the zygomatic that angles slightly above level in the Frankfurt horizontal plane.

Figure 6.50 is a large fragment representing the petrous portion and pterygoid spine. The position of the medial end of the petrous relative to the pterygoid spine

suggests the foramen lacerum was patent and moderate in size. This statement represents the limited analysis that can be completed with such fragments. Burial 87 (Figure 6.51) demonstrates a slight angle to the medial infraorbital margin, and Figure 6.52 (Burial 296, basilar view) the bridging of the right jugular foramen. Figure 6.53 (Burial 310) shows bony spurs on the hard palate in the final example.

Figure 6.46: Perry Site Burial 220

Figure 6.47: Perry Site Burial 111

Figure 6.48: Perry Site Burial 131

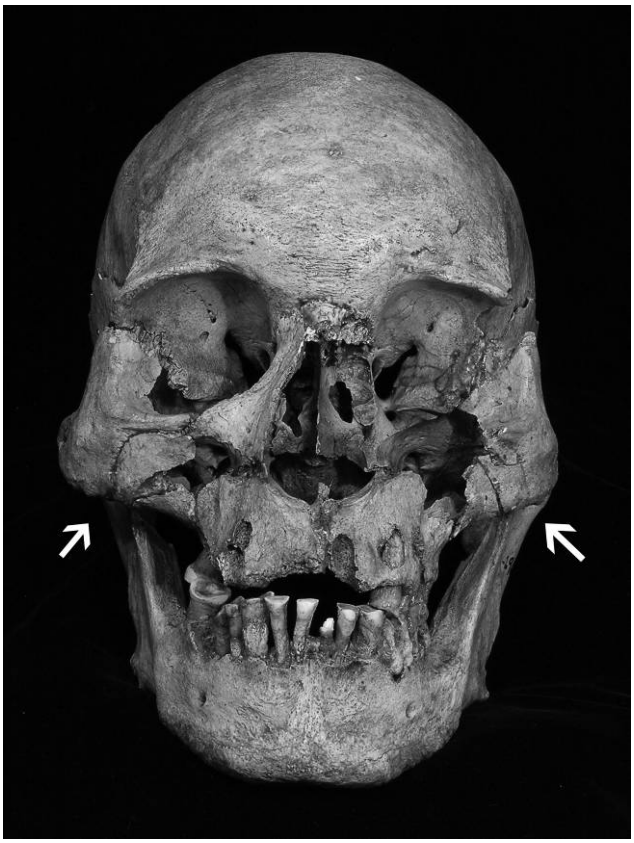


Figure 6.49: Perry Site Burial 296

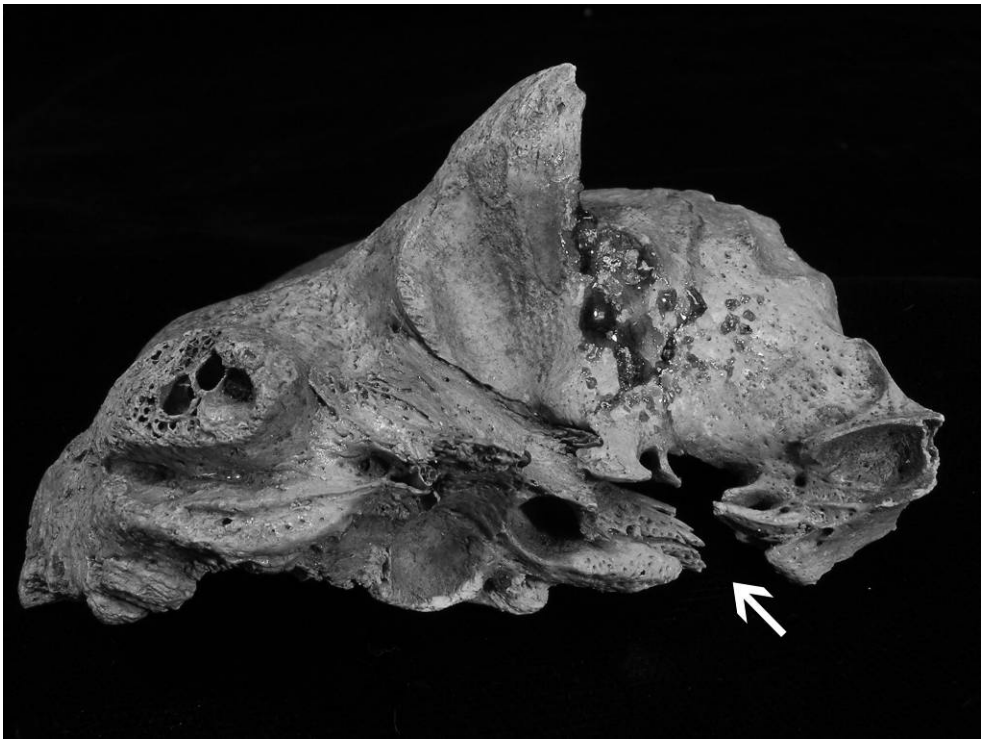


Figure 6.50: Perry Site Burial 254

Figure 6.51: Perry Site Burial 87

Figure 6.52: Perry Site Burial 296

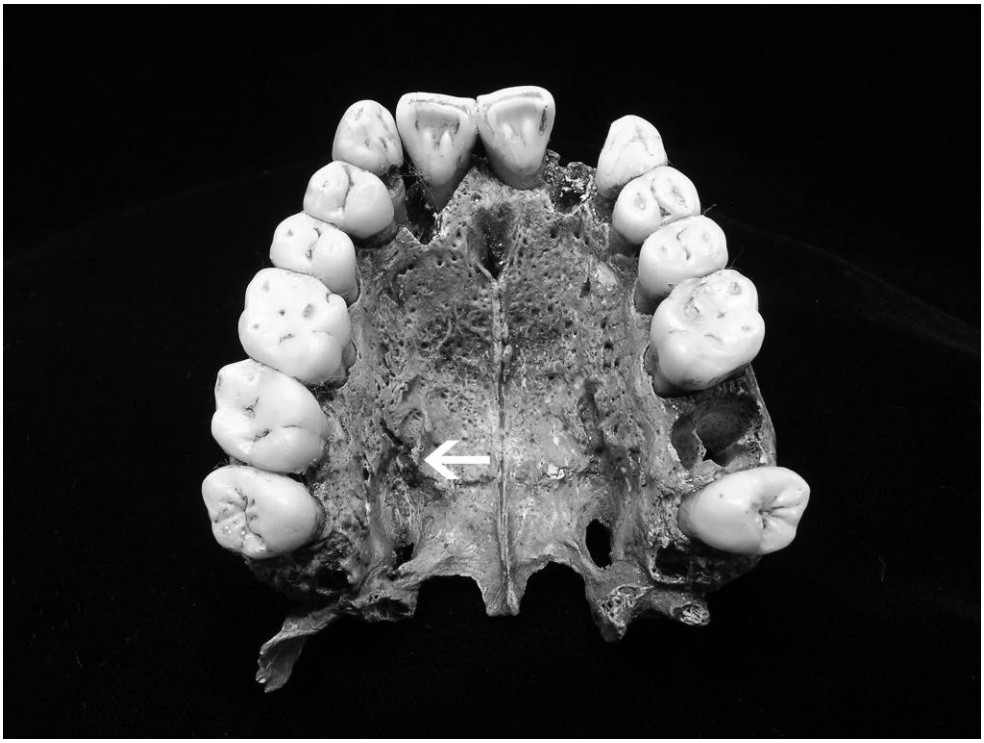


Figure 6.53: Perry Site Burial 310

7.0 DISCUSSION AND CONCLUSIONS

7.1 INTRODUCTION

Cladistic analysis is a means by which to generate testable hypotheses about biological relationships. Specifically, cladistics uses hypotheticodeductive reasoning to understand differences between organisms that are the result of past events – genetic differences that manifest themselves in the phenotype and are fixed in a group of organisms, and presumably only that group. The appearance of the trait in the population is a historical event that demonstrates that the group is unique. Cladistics offers a means to test the differences that arise between groups since these represent historical events. Phenetics, the general set of analytical principles that guide current biodistance analysis, is a means of estimating central tendencies. The group has – in biological terms – become an estimate, and not an entity defined by uniqueness. Therefore, if an experienced osteologist, who uses a phenetic approach, would not be able to associate a cranium with a particular group if its provenance was unknown. To highlight this fact, one needs only to look at the standard practices of forensic anthropologists.

Forensic anthropologists use data that derive from observations on 20th century samples of skeletal material. The resultant formulae have become required applications in most osteological analyses. These formulae are based on traditional North American

cultural groups, commonly called Black, White, and Hispanic (Schwartz, 1995; Stewart, 1979; Ubelaker, 1989). Other studies have provided analytical formulae for Native American groups, but those most widely used are based solely on prehistoric Mesoamerican prehistoric (Genovés, 1967; Schwartz, 1995).

These formulae do not offer a reasonable degree of satisfactory results beyond the borders of North America. For instance, in the forensic research of mass graves involving the Balkans conflict the standard formulae could not delineate local ethnic groups, that almost assuredly did not intermarry (Ross, 2004). Indeed, Ross (2004) acknowledges these limitations and calls for local standards of evaluation. This would require the analysis and determination of the central tendencies of metric and nonmetric characters for every potential group around the world that would be of interest for comparison, as well as to all skeletal samples for which a biodistance analysis would be desired. However, if it were possible to do this, closely related groups may not show statistically significant differences. This sort of analysis would still be subject to the problems of estimating the prominence of specific characteristics and using this average as the defining character of the group to compare to other samples.

Cladistic analysis offers the opportunity to examine any sample in reference to another sample without the need for complete, world-wide estimations of all possible groups. Cladistics also requires biologically defined groups, not culturally defined groups that are used in current biodistance studies.

The ability to use cladistic analysis, however, hinges on the possibility of illuminating characters unique in order to delineate a particular group as a morph.

Without the ability to demonstrate that a suite of characters are the defining phenotypic elements of a particular group, cladistic analysis would not be possible.

7.2 ANSWERS TO HYPOTHESIS AND RESEARCH QUESTIONS

7.2.1 Unique characters in human groups

The answer to the overarching hypothesis of finding unique characters in order to delineate a group for the purposes of cladistic analyses is – It may be possible. The single character not found in other samples was the small bony spur that appears in Spitalfields specimens 2251 and 2278. This may indicate that it is indeed possible to delineate unique characters, but the process is neither simple nor easy and is one that must encompass many coordinated research projects of like-minded individuals focusing on finding these characters and comparing a large amount of descriptive data, as is typical in any paleontological analysis and debate.

Currently, the demands of pursuing a cladistic analysis to determine biological distance between groups of humans, even if possible, would require too many resources and too much time to be a reasonable line of research. This does not mean, however, that osteologists and bioarchaeologists should stop thinking about and conducting biodistance analysis. We should seek to improve our knowledge of the biology behind the morphology to better understand the subtle phenotypic differences that could be used to delineate morphs to use in biodistance analysis.

7.2.2 Level at which unique traits present themselves

The issue of possibility and difficulty of illuminating unique characters and delineating morphs in biodistance analysis may be tied to the biological level of the group. For systematists and other biologists, the only "true" biological group in nature is the species. This interpretation derives in part from the belief that only members of a species can breed with each other, creating a natural genetic boundary, and that by recognizing each other as potential breeding mates, the individuals define their species (Mayr, 1982; Patterson, 1985). Therefore, all other taxonomic levels are theoretical extensions based on what and how many unique characters are shared between organisms of different species (see Chapter 4). This theoretical extension of taxonomy beyond the species level also holds for any subspecific groups or populations. This level – below the species – of analysis has traditionally been completed by phenetic methods (Wiens, 1999). Variation, and not diversity, is the focus of for determining subspecific groups, including human groups.

The "maybe" answer to the main hypothesis shows that the uncovering of unique traits that might reflect diversity within a species has promise. I do submit, however, that the human species has a different aspect than most species in terms of judging diversity and variation: humans are found all over the globe. This is a problem because often, in judging differences within a species of any other organism, geography is a deciding factor in determining these subspecific groups (Mayr, 1970). While geography has been used to support ideas of differences between human populations, it is not reasonable to use geography to delineate human groups.

No character presented in this study, or otherwise, seemed to be associated with a specific family group of named individuals (Appendix G). While finding or not finding characters delineating family groups within the sample is not one of the questions asked in this project, it is interesting to note that no characters delineated family groups. This is not surprising, however, as family groups are only representative of the variation to be found within a sample, just as a population only represents part of the variation of the overall species.

This project, however, focuses on the level at which typical biodistance analysis is conducted – at the sample level, usually archaeologically derived. It may be possible to distinguish morphs at a level lower than the species, but higher than the small populations that are the usual focus of biodistance analysis.

7.2.3 Using less-than-well preserved specimens and samples

Skeletal samples recovered from the archaeological record are rarely found in perfect condition, because of the digenetic affects of the soil matrix in which they are buried, skeletal elements are recovered in varying conditions, ranging from almost pristine to unidentifiable fragments. Given the results of the comparative analysis of this thesis, it appears use of archaeological samples for comparative cladistic analyses requires a large number of relatively well-preserved specimens. This is generally the case for the comparison of archaeologically recovered skeletal remains, for metric as well as nonmetric types of analyses. For biodistance, many specimens preserved well enough for thorough examination are needed no matter the method used for the determination of biological relatedness.

For nonmetric traits, preservation issues may be less critical than for measurements. Why? While only the portion of the element that has the character(s) of interest is needed for nonmetric analysis, the entire element is needed to complete an accurate metric analysis. This difference between nonmetric and metric analysis has been used to argue a preference for the use of nonmetric traits in biodistance analysis. Even so, the preservation of the skeletal elements must be good enough to facilitate the direct comparison of characters.

7.3 IMPLICATIONS FOR THE STUDY OF FOSSIL HOMINIDS AND OTHER GROUPS

The same questions about the study of recent *Homo sapiens* skeletal material also apply to the systematic study of the human fossil record. The phenetics/cladistics debate originated in paleontological study, and directly affects research of the evolutionary relationships of hominids.

The results of this study demonstrate that it is unlikely that unique morphological characters can be found that will delineate a human morph at the subspecific level. While this project exclusively focused on relatively recent (in evolutionary terms) specimens of *Homo sapiens*, the results have implications for studies of fossil hominids. Specifically, the results suggest unique traits found in fossil hominids do not represent variants of a broader group (species). It is much more likely that the unique morphology is indicative of a morph that represents a unique species. If we do not find unique characters in modern human populations, even those groups that are relatively

genetically isolated, then why should paleontologists argue that fossil that have unique characters are not morphs, or representative of a different species, are just variation and not part of a diverse pattern of different species?

Another issue that should be addressed when considering the possibility of delineating groups of humans by morphology is the affect that a positive or negative result may have on how researchers view specimens recovered from the fossil record. The multiregional hypothesis is an alternative to the view that humans evolved in Africa and migrated to other parts of the globe. The multiregional model sees the evolution of modern humans as having happened everywhere because each geographic region was part of the whole of evolutionary geography (Stringer, 2001; Thorne and Wolpoff, 1992). The multiregional view is that ancient hominids, such as *Homo erectus* (Wolpoff et al., 1984), are variants of *Homo sapiens* and that the evolutionary history of humans is one of intertwined, genetically linked populations, with hominids such as *H. erectus* and *H. neanderthalensis* contributing to the gene pool of modern humans (Churchill and Smith, 2000; Thorne and Wolpoff, 1992). According to the multiregional argument differences between modern human populations result from the overall adaptive plasticity of humans being affected by local selection pressure, not multiple regional origins of *Homo sapiens* (Tattersall, 1997; Wolpoff, 1989; Wolpoff et al., 2000; Wolpoff et al., 1984).

Because fossil hominids and extant humans are viewed as sharing in a genetic/biological continuum (Stringer, 2001), one of the central themes of the multiregional model is that recent human regional populations also display a morphological continuum with non-extinct hominids (modern humans) of the same regions (Lahr, 1996; Wolpoff, 1989; Wolpoff et al., 1984). Thus, the multiregional model

counts only the minimum number of species because hominid fossils, specifically those of the genus *Homo*, are viewed as representing a range of general human variation.

The multiregional model proposes that the fossil hominids a preserved range of variation found in all humans, and should therefore be considered in the range of variation found in extant humans. For the assertion that specimens of fossil hominids fall within the range of normal human variation to be true, no unique character should be found in any given specimen. However, there seems to be a considerable number of unique characters that can be used to delineate hominid fossil morphs. These unique character states are not found in modern humans or any other hominid specimen. There are many familiar examples of unique characters found in fossil hominids that are not found in extant humans. For instance, the shelf-like brow and "hamburger bun" shape of *H. erectus* exemplified by the Trinil 2 skull and the occipital bun and the retromolar space of the mandible in *H. neanderthalensis*, which can be seen in the Tabun I specimen (Schwartz and Tattersall, 2003; Tattersall and Schwartz, 2000). New characters that delineate these species are being discovered, as with the nasal cavity medial projections found in *H. neanderthalensis* specimens such as those from Forbe's Quarry (Gibraltar) and other specimens where the nasal region has been preserved (Schwartz and Tattersall, 2002; Tattersall and Schwartz, 2000).

A fundamental problem with the idea of a multiregional development of modern humans is that the observed continuity of characters assumes that the observed traits are gradients of the same character. This assumption ignores the basic premise that primitive and derived characters, even if orthologous, reflects diversity and not variation. For instance, an argument has been made that the supraorbital torus that is so

distinctive in Neanderthals is part of a morphological continuum that includes fossil specimens of *H. sapiens* from central Europe (Smith et al., 1989). While statistics show that the thickness of the torus (if such can be recognized in modern humans) is continuous, it ignores a key element. It is the shape of the character that is of evolutionary significance.

Analysis that supports the multiregional hypothesis generally uses the frequency of the appearance of specific traits to try and demonstrate regional continuity. But given a frequency analysis of a broad sample of the morphology human skeletal material, specifically those traits that are considered to be key to the regional argument (Thorne and Wolpoff, 1981; Weidenreich, 1946), the results do not support an argument for regional continuity of morphological characters.

Lahr (1996) clearly demonstrates that there is no morphological basis for the multiregional model in her analysis of the characters used to argue for regional continuity between different fossil and extant hominids. No traits that presented in the multiregional model are exclusive to any humans of any region of the world. In addition, traits used in the multiregional model do not demonstrate a gradient of expression. As Lahr (1996:151,154) concludes, “most of the regional features used as evidence of multiregional evolution are actually ancestral for all modern humans.”

This statement further demonstrates the conflation of variation within a group (species) and diversity between groups exemplified by arguments such as the multiregional model. This conflation also exists in the morphological analysis of extant human groups. Combined, the ideas of the multiregional model become inevitable, with morphological traits seen as continuous from fossil to extant humans in their respective

regions of the world. The results of this project support the conclusions made by Lahr that so-called regional features are common (and ancestral), and thus ancestral to humans in general, further highlighting the problems of how researchers delineate different groups of extinct and extant humans. While it is convenient, and perhaps even a bit idealistic, to view extant and extinct humans as part of a biological continuum represented by shared characters; this view, however, is not reflected in the morphology of the skeletal remains of different hominids. By homogenizing large groups of hominids through paradigms such as the multiregional model, researchers are blurring important boundaries that illuminate human evolutionary history.

7.4 DEVELOPMENTAL GENETICS, CHARACTER FORM, AND FUTURE RESEARCH

If cladistics is a reasonable foundation for future biodistance studies, and for characters to be identified as unique, the etiology of the characters must be better understood. Specifically, the prominent ideas from developmental genetics offer the best chance to understand how skeletal traits form, and what genes are important in the biological relationships of human groups. Recent research in developmental genetics has shown that the control of the appearance of specific traits or suites of traits is the critical aspect of morphological analysis in human evolution (Lovejoy et al., 1999; Schwartz, 2005). The genetics that instruct the development of physical characters must be considered in all aspects of human skeletal analysis, or research of the morphology of human skeletal

material will continue to be directed by the data (Lovejoy et al., 1982), and continue to stagnate.

The concept of growth and development affecting ideas of evolution and classification came to the forefront of biological debate in the late 1970's with Gould's book *Ontogeny and Phylogeny* (1977). While the importance of growth and development is still debated in evolutionary studies (Raff, 1996; Schwartz, 1999c), the debate seems to have been ignored by anthropologists, with a few notable exceptions (Lovejoy et al., 1996; Lovejoy et al., 1999; Schwartz, 1999b; Schwartz, 1999c; Schwartz, 2005). Other anthropologists who do focus on growth and development are content to use general ideas about growth (O'Higgins and Vidarsdottir, 1999), but without considering the genetics of development. Even when the importance of ontogeny is emphasized in studies of growth, the questions are generally about the rates of growth and what they mean in hominid evolution, paleopathology, or paleodemography (Hoppa and FitzGerald, 1999), rather than about how differences in ontogeny are reflected in the differences in morphology.

As understanding about how genes control growth increases, osteologists will be better able to understand what makes the human skeleton what it is. Even without explicit knowledge of how control genes work in skeletal development the concepts of developmental genetics can help physical anthropologists/skeletal biologists formulate better and more appropriate questions regarding analyses of skeletal morphology.

7.5 FINAL THOUGHTS

This project seeks to highlight the problems of current biodistance analysis, and to offer a possible remedy in the form of a cladistic based analysis. The result of the testing of the hypotheses that are the backbone of this thesis is mixed. It may be possible to find characters that delineate morphs within *H. sapiens*. But the level of the analysis at which this can be accomplished is a point of significance. For instance, some characters seem to indicate possible morphs at a large, general population level (Schwartz, unpublished data), whereas this project indicates it is highly unlikely for small populations.

Even if morphs could be delineated at the level of a small population, one question that must be asked is, is it practical? Is biodistance analysis as a whole practical, given the quality of information that osteologists can get from such analyses. The effort and time that it will take to elucidate unique skeletal characters specific to skeletal samples may be much more costly than the returns given the usual nature of skeletal analyses – not to mention the effort it would take to change the perspectives of enough physical anthropologists to make cladistic-based analyses to generate numerous and good-quality comparisons.

Even with the traditional listed characters used in biodistance analyses, the effort to put major human groups in perspective using traditional biodistance methods is, in my opinion, limited (Hanihara et al., 2003). As comprehensive as Hanihara and Ishida's (2001a; 2001b; 2001c; 2003) analyses are, they still begin with groups of people that have been defined by criteria other than their biology, which reinforces cultural typologies, and not establish biological ones.

But until such time that genetic analysis becomes less fraught with questions and researchers have a better grasp of what characters are controlled by which genes, biodistance analysis should, perhaps, defer to other types of data, such as artifact analysis, when seeking answers to archaeologically significant questions about migration, endogamy/exogamy, and patrilocal/matrilocal mating patterns. Even other data that can be obtained from skeletal material, such as isotope analysis, may be preferable to using biodistance analysis in its present state (e.g. Schulting and Richards, 2001).

In short, biodistance analysis, in its current state, is too flawed to be used to accurately answer questions about the biological structure of human groups.

APPENDIX A

COMPARATIVE DATA COLLECTED FROM THE SPITALFIELDS SAMPLE

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Posglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2004		49	F	-	-	-	MR	-	-	-	S	-	-	0	-	0	-	M	+	+	-	0	-	SD	SD
2008		40	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2022		40	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
2024		54	M	-	W/0	-	L0	-	S	-	S	0	M	0	-	0	L	-	-	-	-	-	EVEN	-	-
2027		58	M	N/0	-	MR	-	L	-	S	S	-	-	-	S	-	-	-	0	0	0	0	-	SS	-
2063		92	M	W/0	W/0	MO	MO	M	M	S	S	0	-	0	S	0	S	S	0	0	0	0	BEHIND	OS	OS
2066		78	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2070		35	F	N/0	-	MO	MO	L	M	S	S	0	0	0	L	0	L	S	S+	S+	S+	S+	BEHIND	OS	OS
2079		29	F																						
2098		80	F	W/0	W/0	LO	LR	M	L	M	L	0	0	0	M	0	M	S	S+	S+	S+	S+	EVEN	OS	RS
2099		68	F	W/0	W/0	LO	LR	M	M	S	S	0	0	0	M	0	M	+	+	+	+	+	BEHIND	SS	SS
2104		16	M	W/0	W/0	-	LO	M	M	-	S	0	-	0	-	0	L	S+	S+	S+	S+	S+	BEHIND	SS	SS
2108		72	F																						
2111		49	F																						
2112		18	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2126		76	F																						
2129		67	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2134		89	F	W/0	W/0	MO	MO	S	S	M	M	0	M	M	0	0	M	M	+	+	+	+	BEYOND	SS	SS
2137		62	F	-	-	-	-	-	-	-	-	-	-	?	-	0	M	-	-	-	-	-	-	-	-
2139		10	M	W/0	W/0	MR	MO	S	M	M	M	0	?	?	0	0	M	M	+	+	+	+	?	SS	SS
2142		27	F	N/0	N/0	MO	MO	S	S	S	S	0	0	M	0	0	M	M	S+	S+	S+	S+	EVEN	OS	OS
2149		44	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2152		87	F	W/0	W/0	LO	LO	M	M	M	M	0	0	0	0	0	M	M	0	0	0	0	EVEN	SS	SS
2157		77	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2004	-	N	N	L/I/M	L/I/M	+	S+	BN	-	A	-	+	+			Metopic suture patent
2008	-	N	N	L/M	-	-	-	-	-	A	-	-	-	-	-	Badly damaged
2022	-	B	B	L/I/M	L/M	+	+	LD	LD	A	A	0	0	-	-	Basicranium badly damaged
2024	-	N	N	-	-	-	-	-	-	-	-	-	-	-		Left side damaged
2027	THINPOINT	-	N	-	-	-	-	-	-	-	-	-	-	-	-	2 supraorbital notches on right
2063	?	N	F	L/I/M	L/I/M	S+	S+	LN	LD	SA	SA	0	0			
2066	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2070	THICKPOINT	F	B	L/I/M	L/I/M	S+	S+	LD	LD	SA	SA	0	+			Left ovale divided within foramen
2079																Missing
2098	MODPOINT	N	N	L+/I	L/I/M	+	+	BD	BD	SA	SA	0	0			
2099	MODBLUNT	B	B	L/I	L/I/M	+	+	LD	BD	L	L	0	0			Advanced sphenoid spine ossification
2104	MODSQUARE	-	-	-	-	-	?	-	?	?	SA	-	-	-	-	
2108																Missing
2111																Missing
2112	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Crumbs
2126																Missing
2129	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2134	MODSQUARE	N	N	L+/I	L+/I	++	++	LD	LD	L	L	0	0			Advanced sphenoid spine ossification
2137	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
2139	THINSQUARE	N	N	L/I/M	L/I/M	S+	+	LD	LD	L	L	0	0			Advanced sphenoid spine ossification
2142	MODBLUNT	N	N	L/I/M	L/I/M	S+	S+	BD	BD	L	L	+	0			
2149	-	F	-	L+/I/MI	-	S+	-	-	-	A	-	0	0	-	-	Badly damaged
2152	MODBLUNT	N	N	L/I	L/I/M	+	0	UN	UN	SA	SA	0	0			Advanced sphenoid spine ossification
2157	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2158	41	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	S+	-	-	-	-	RS
2162	58	M	W/0	W/0	MO	MO	M	M	L	L	0	M+	M+	0	0	S	S	+	+	++	++	EVEN	OD	OD
2163	19	M	N/0	DAM/0	MO	DAM	M	-	M	-	+S	0	0	0	0	M	-	+	+	+	+	BEHIND	SS	SS
2166	70	F	N/0	N/0	MO	MO	S	S	VS	VS	0	M	M	0	0	M	M	+	+	0	0	EVEN	SS	SS
2167	68	M	W/0	W/0	MO	MO	S	S	M	M	0	M	M	0	0	M	M	+	+	+S	+S	BEYOND	OD	OD
2169	85	F	M/0	M0	LO	SO	S	S	VS	VS	0	M	M	0	0	M	M	+	+	+S	+S	BEHIND	OS	RS
2171	58	M	DAM/0	DAM/0	MO	MO	S	S	M	M	0	0	0	0	0	S	S	+	+	+	+	BEHIND	SS	SS
2173	40	M	W/0	W/+	MR	MO	L	L	L	L	+	M	M	+	+	L	L	-	+	-	-	BEYOND	-	-
2175	15	F	W/0	W/0	MO	MO	S	S	M	M	0	0	M?	0	0	M	M	+	+	+S	0	BEHIND	SS	RS
2176	59	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2178	36	M	W/0	W/0	LO	LO	S	S	L	L	0	0	M	0	0	M	M	0	0	0	0	EVEN	OS	OS
2181	64	M	DAM/0	DAM/0	MO	MO	S	S	L	L	0	DAM	DAM	0	0	M	M	0	0	0	0	EVEN	OS	SS
2182	70	M	W/0	W/00	LO	LR	M	?	M	M	0	0	0	+	0	M	M	+	+	+S	+S	BEHIND	OD	OS
2184	68	F	W/0	W/0	LO	MO	S	S	M	M	0	0	0	0	0	L	L	+S	+S	0	0	EVEN	SS	SS
2185	32	M	-	-	SR	-	VS	-	S	S	+DOUBLE	0	0	0	0	-	-	-	-	-	-	-	-	-
2186	51	M	VW/+	VW/0	LR	LO	S	S	M	DAM	0	S?	S?	0	+	M	M	+S	+S	0	0	JBEHIND	RD	RD
2187	31	M	W/0	W/0	MO	MO	M	M	M	L	0	0	0	0	0	M	M	+S	+S	+	+	EVEN	RS	RS
2189	55	F	W/0	W/0	LO	LR	M	M	M	L	VS	0	0	0	0	L	L	+S	+S	+	+	BEHIND	RS	RS
2192	63	F	N/0	N/0	MO	MO	S	S	S	M	0	0	0	0	0	M	M	+	+	0	0	EVEN	SS	SS
2203	58	M	W/0	W/0	LO	LO	M	M	S	S	0	0	0	0	+	L	L	+	+	+	+	BEYOND	OD	OD
2204	78	F	N/0	N/0	SO	SO	M	L	M	M	0	0	0	0	0	S	S	+S	+S	0	0	BEHIND	RS	RS
2205	57	F	N/0	N/0	MO	MO	S	S	M	S	0	0	0	0	0	M	M	+	+	+	+	BEHIND	SD	SD
2207	63	M	N/0	N/0	MO	LR	S	S	S	S	0	0	M	0	0	M	L	+S	+S	+S	+S	BEHIND	OD	OD
2211	62	M	N/0	N/0	MO	MO	S	S	M	S	0	0	0	0	0	S	S	+S	+S	+S	+S	EVEN	OD	OD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2158	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2162	THICKSQUARE	B	B	L/I/M	L+/I/M	++	++	LD	LD	SA	SA	0	0			Slight palatal torus med/lat, skinny
2163	MODBLUNT	N	B	L/I/M	L/M	0	0	UN	UD	SA	SA	0	0			Notches in infraorbital margins
2166	MODSQUARE	N	F	L+/I/M	L+/I/M	++	++	LD	LD	L	L	0	+			Wide growth on right sphenoid spine
2167	MODBLUNT	N	N	L/I/M	L/I/M	+	+	UD	UD	SA	SA	0	0			Right sphenoid spine growth; right spenoid spine almost bridged
2169	MODSQUARE	B	B	L+/I/M	L+/I/M	++	+	LD	LD	A	A	0	0			Loop of bone over left f. spinosum
2171	MOD/DAM	?	?	L+/I/M	L+/I/M	+	+	LD	LD	L	L	0	S+			
2173	-	F	B	L+/I/M	L+/I/M	+S	+S	BD	BD	SA	SA	0	0			Extreme growth on left spehnoid spine; med. orbital wall macroporosity; r. lat. sph. plate foramen
2175	MODPOINT	F	F	L/I/M	L/M	0	0	UN	-	L	L	0	0		-	Wide growth on right sphenoid spine, almost bridged
2176	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2178	MODBLUNT	N	N	L/I/M	0/I/M	0	0	UD	UD	L	L	0	0			Wide growth on sphenoid spine; thyroid cartilage ossifed
2181	THINFLAT	N	DAM	L/I/M	L/I/M	0	0	LD	LD	SA	SA	+	0			Sphenooccipital not fused; both jugular foramina almost completely closed off
2182	THICKSQUARE	N	N	L/I/M	L/I/M	0	0	UD	UD	SA	SA	0	0			Right ovale only bridged; lots of hyperostsotic activity on sphenoid spines; very broad face
2184	MODSLPOINT	N	N	L/I/M	L/I/M	0	0	LD	LD	A	A	0	0			Right spinosum bridged; very narrow face
2185	-	-	B	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged; left and right spur at basion
2186	MODBLUNT	N	N	L+/I/M	L+/I/M	++	++	BD	BD	A	A	0	0			Right ovale almost bridged
2187	THICKPOINT	N	N	L/I/M	L/I/M	0	0	BD	BD	SA	SA	0	0			Palate bone wing-shaped
2189	MODSLPOINT	F	B	L/I	L/I/M	0	0	LN	LN	SA	SA	0	0			Growth on right sphenoid spine; formane in right lateral sphenoid plate
2192	MODSLPOINT	N	F	L+/I/M	L+/I/M	++	++	LD	LD	SA	SA	0	0			Palatal torus
2203	MODSQUARE	B	F	L/I/M	L/I/M	+S	+S	DAM	LN	SA	SA	0	0			Extreme growth on sphenoid spine; deep palate
2204	THICKPOINT	F	N	L+/I/M	L+/I/M	+	+V	UN	UN	L	L	O	O	?	?	Cloth adhering to zygomas
2205	THINPOINT	N	N	L+/I/M	L+/M	++	++	UN	LN	A	A	0	+			Greater palatine foramina wide, deep slits
2207	THICKSLSQ	N	F	L+/I	L/I/M	+	+	UD	UD	A	A	0	0			Ridge/torus down center of palate
2211	MODSLSQ	B	B	-	-	+	-	U-	-	A	-	0	0	-		Accessory supraorbital foramen, small

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2216	61	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2221	64	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2223	49	M	-	-	MR	MR	S	S	L	L	0	M	M	0	0	S	S	0	0	0	0	EVEN	-	-
2231	72	F	W/+	W/0	LO	LO	M	M	M	M	0	0	0	0	0	M	M	0	0	0	0	EVEN	OD	OD
2240	53	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OD	-
2243	67	F	-	-	MO	MO	S	S	M	M	0	0	0	0	0	S	S	-	-	-	-	EVEN	-	-
2244	64	M	W/0	W/0	MO	MO	M	M	L	L	0	0	0	0	0	M	M	+S	+S	0	0	EVEN	RD	RD
2246	86	F	N/0	N/0	MR	LR	-	S	S	M	+	0	0	0	0	L	L	0	0	0	0	BEHIND	OD	OD
2251	D	F	N/0	N/0	SO	MR	S	S	L	M	+	0	0	0	0	L	L	0	0	0	0	BEHIND	OS	OS
2254	34	M																						
2255	36	M	W/0	W/0	MO	MO	M	M	M	M	0	0	0	0	0	M	M	+S	0	0	0	EVEN	SD	OS
2259	48	F	W/+	W/0	MO	LR	M	M	M	S	0	0	0	0	0	S	S	+S	+S	0	0	BEHIND	SS	SS
2263	73	F	-	N/0	-	SO	-	M	-	-	-	-	-	-	-	L	M	0	0	-	0	-	-	SS
2267	82	F																						
2272	87	F	N/0	N/0	MO	LR	M	S	L	M	+	M	M	0	0	M	M	0	0	0	0	EVEN	OD	OD
2281	34	F	DAM/0	DAM/0	MO	LR	M	S	M	M	0	0	0	0	0	L	L	0	0	-	0	EVEN	SS	SS
2284	47	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2286	34	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2291	61	M	DAM/0	W/0	LO	MO	M	M	M	M	0	M	M	0	0	L	L	0	0	0	0	EVEN	SS	SS
2292	26	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2295	61	F	N/0	N/0	MO	MO	M	M	M	S	0	0	0	0	0	M	M	+S	+S	0	0	EVEN	OS	OS
2296	39	F	N/0	N/0	MO	MO	M	M	M	M	0	0	0	0	0	L	L	+S	+S	+S	+S	EVEN	RS	RS
2298	58	F	N/0	W/0	MO	MO	M	M	S	M	0	0	0	0	0	S	S	+S	+S	0	0	EVEN	OD	OD
2300	53	F	N/0	N/0	MO	MO	S	M	M	M	0	M?	M?	0	0	S	S	0	0	0	0	BEHIND	SS	SS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2216	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged, barely anything left
2221	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly damaged; thyroid cartilage ossified
2223	-	N	N	-	-	-	-	-	-	-	-	0	0	-		Badly damaged
2231	MODFLAT	N	N	L/I/M	L/M	0	0	LD	LD	SA	SA	0	0			Sphenoid spine growth; left spinosum bridged; odd jugular foramina
2240	-	N	B	-	-	-	-	-	-	-	-	-	-	-	-	Dammaged, possibly droppped
2243	-	N	B	-	-	-	-	-	-	-	-	0	+	-	-	Extensive taphonomic damage
2244	MODBLUNT	N	-	0/I/M	-	+	-	DAM	DAM	A	-	0	0	DAM	-	Damaged
2246	THICKSQUARE	N	N	L/I	L/I	0	0	UD	UD	SA	SA	0	0			Huge infraorbital formaina; thyroid cartilage ossified
2251	MODBLUNT	N	N	DAM	L/M/I	DAM	++	DAM	LD	A	A	0	0	DAM		
2254																
2255	MODSQUARE	B	B	L/I/M	L/I/M	0	0	UD	UD	SA	SA	0	0			Supraorbital nothces and accessory foramen present
2259	MODSLPOINT	N	N	L/I/M	L/I/M	++	++	LD	LD	L	L	0	0			Sphenoid spine growth
2263	DAM	N	N	-	L+/I	-	++	-	UN	SA	SA	0	0		-	Damaged
2267																
2272	MODBLUNT	N	N	L/I	DAM	++	++	LD	LD	A	A	0	0			
2281	-	B	B	-	-	-	-	LN	-	-	-	0	0	-	-	Damaged
2284	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extensive taphonomic damage
2286	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extensive taphonomic damage
2291	MODCURVESQ	N	N	L+/I/M	L+/I/M	DAM	DAM	LD	DAM	SA	SA	0	0			
2292	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extensive taphonomic damage; growth on sphenoid spine; thyroid cartilage ossified
2295	MODSLPOINT	N	N	L+/I/M	L+/I/M	+	+	LD	LD	A	A	0	0			Supraorbital nothces and accessory foramen present
2296	MODPOINT	N	F	L/I	L/I	0	0	UD	UD	L	L	0	0			
2298	MODSLPOINT	B	B	L/I/M	L+/I/M	+	+	UN	UN	A	A	0	+			
2300	MODSLBLUNT	B	B	L+/I/M	L+/I/M	++	++	LD	LD	A	A	0	0			

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2301	35	F	N/0	N/0	LR	MO	M	M	S	S	+	0	0	0	0	L	L	0	0	0	0	BEHIND	SS	OS
2304	64	M																						
2308	18	F	DAM/0	N/0	SO	SO	S	S	M	-	0	0	-	0	-	S	-	0	0	0	0	VBEHIND	RS	RS
2309	77	F																						
2327	23	F	N/0	N/0	SO	MO	S	-	M	M	0	0	?	?	L	L	L	S+	S+	-	-	EVEN	RS	RS
2330	75	M																						
2335	75	F	N/0	N/+	MR	MR	M	M	VS	VS	0	0	0	0	0	M	M	0	0	0	0	EVEN	OS	OS
2337	11	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2340	54	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2344	53	M																						
2360	83	M	DAM/0	DAM/0	MO	MO	-	S	-	M	0	-	-	-	0	-	-	+	+	+	+	EVEN	OS	RS
2363	61	M	N/0	N/0	MO	MO	L	L	M	M	0	0	0	0	0	L	L	+	+	+S	+S	EVEN	OS	RS
2368	45	F	N/0	N/0	LO	LO	M	S	M	S	0	0	0	0	0	M	M	+	+	0	0	EVEN	OS	OS
2369	55	F	W/0	W/+	MO	MO	L	L	?	?	?	0	0	0	0	M	M	+	+	0	0	?	OS	OS
2371	67	F	N/0	N/0	MO	MR	S	S	M	M	0	0	M	0	0	L	L	+S	+S	+S	+S	EVEN	RS	OS
2372	53	F	N/0	N/0	LO	LO	M	M	M	M	0	0	0	0	+	M	M	0	0	0	0	BEHIND	SS	SS
2381	22	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2382	52	F	N/0	N/0	LR	LR	M	L	M	M	+	0	0	0	0	M	M	0	0	0	0	BEHIND	OS	OS
2389	39	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2399	29	F	DAM/+	DAM/0	MO	MO	M	M	L	L	0	0	0	0	0	M	M	0	0	0	0	VBEHIND	SD	SD
2400	34	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2401	47	M	N/0	N/0	-	-	-	-	-	-	0	-	-	-	-	-	-	+	+	+	+	BEHIND	RD	RD
2402	32	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2406	70	M	DAM/0	DAM/0	MO	MO	M	M	M	S	0	M	M	0	+	L	L	+S	+S	0	0	BEHIND	OS	OS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2301	MODSLBLUNT	N	N	L/I/M	L/I/M	0	0	LD	LD	SA	SA	0	0			
2304																
2308	MODFLAT	-	-	-	-	-	-	-	-	-	-	-	0	-	-	Damaged
2309																
2327	THIN/DAM	N	N	L/I/M	L/M	+	+	LD	LD	SA	SA	0	+			Sphenoid spine growth
2330																
2335	MODFLAT	N	N	-	L/M	0	0	-	UN	A	A	0	0		-	Right foramen spinosum bridged; very narrow face
2337	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extensive damage, only crumbs and dust
2340	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
2344																Missing
2360	MODSQUARE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged; spur @ massive f. magnum; spur over R spinosum - almost bridged
2363	MODBLUNT	N	F	L/I/M	L/M	0	0	LD	LD	A	A	0	0			Sphenoid spine growth; growth of lateral pterygoid plates
2368	MODFLATSQ	N	N	L/I/M	L/M	+	+	LN	LN	SA	SA	+	0			Narrow, level zypomatic arches
2369	MODFLATBL	F	F	L+/I/M	L+/I/M	+	+	BD	BD	SA	SA	0	+			R. Pterygospinous bridge; growth on left sphenoid spine; dessicated flesh obscuring some features
2371	LGFLATBLUNT	N	N	L++/I/M	L++/I/M	++	++	LN	LN	A	A	0	0			Heavy lipping on infraorbital foramen
2372	MODFLAT	F	F	L+/I	L+/I	++	++	LD	LD	L	L	0	0			Huge fissures in orbit floors
2381	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Heavily damaged
2382	MODFLATBL	B	B	L/I/M	L/I/M	+	+	LN	LN	SA	SA	0	0			R. jugular foramen almost bifurcated; posterior palatal margin wavy-shaped
2389	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Heavily damaged
2399	MODPOINT	N	B	L+/I/M	L+/I/M	+	+	LN	LN	L	L	-	0			Left spinosum bridged; great deal of growth on sphenoid spine
2400	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Heavily damaged
2401	MODSLPOINT	-	-	-	-	-	-	LN	-	-	-	0	-	-	-	Heavily damaged
2402	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extensive taphonomic damage; dust and crumbs
2406	LGBLUNT	N	N	L/I/M	L/I/M	0	0	UD	UD	SA	SA	0	0			Right spinosum axis posterior; sphenoid spine growth

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2407		65	F	W/0	W/0	MO	MO	M	M	M	L	0	0	0	0	0	L	L	0	0	+	+	BEHIND	SD	SD
2414		60	F	DAM/0	DAM/0	MO	MO	M	L	M	M	0	0	0	0	0	L	L	+	+	++	++	BEHIND	RS	RS
2418		68	M	N/0	N/0	MO	MO	L	M	S	S	+	0	0	+	0	M	M	0	0	0	0	EVEN	RS	SS
2419		63	M	W/0	W/0	MO	MO	M	M	L	L	0	M	0	0	0	L	L	0	0	0	0	EVEN	OD	OD
2424		56	M	-	-	SO	-	S	-	S	L	0	0	0	-	0	M	M	-	-	-	-	-	-	-
2430		90	M																						
2432		47	F	-	-	LO	-	S	S	M	M	0	0	0	+	0	L	L	-	-	-	-	EVEN	-	-
2437		57	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2438		56	F	N/0	N/0	MO	MO	S	S	S	-	0	S	-	-	-	-	-	0	0	0	0	BEHIND	SD	SD
2439		65	M	DAM/0	DAM/0	LO	LO	M	M	L	M	0	0	0	0	0	M	M	0	0	0	0	BEHIND	OD	OD
2442		71	M	DAM/0	DAM/0	LR	LO	M	M	M	M	0	M	0	0	0	M	M	+	+	0	0	EVEN	OD	OD
2445		32	M	-	-	MO	-	S	M	S	M	0	M	0	++	+	L	L	+	+	+	+	EVEN	OD	OS
2449		74	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2458		51	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2459		29	F	-	-	LR	-	S	S	M	-	+	0	0	0	-	M	L	-	-	-	-	-	-	-
2461		74	M	-	-	LO	LO	M	M	M	M	0	M	M	+	0	M	M	-	-	-	-	DAM	-	-
2463		45	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2464		91	M	W/+	DAM/0	MO	MO	M	S	M	M	0	0	0	0	0	L	L	0	0	-	-	EVEN	OD	DAM
2465		26	F	N/0	N/0	MO	LR	M	S	M	S	0	0	0	0	0	S	S	+S	+S	+S	+S	EVEN	RS	OS
2467		56	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2468		50	M	-	-	MO	-	M	S	-	-	0	0	-	-	-	S	M	0	0	-	-	-	-	RD
2469		53	M	-	-	LR	LR	M	M	L	M	0	0	0	0	0	L	L	-	-	-	-	EVEN	OD	OD
2470		57	F	-	-	LO	LO	S	S	-	-	0	-	-	-	-	M	-	-	-	-	-	-	-	-
2471		41	F																						

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2407	MODBLUNT	N	F	L++/I	L++/I	+	+	LN	LN	A	A	0	0			Sphenoid spine growth; R. ovale almost bridged; both jug. ff. almost bifurcated; huge vaginal procs.
2414	MOD/DAM	N	N	L/I/M	L/I/M	+	+	BD	BD	L	L	0	0			Sphenoid spine growth; left ovale almost bridged
2418	FLATSQUARE	F	B	L+/I/M	L/I/M	0	+	UD	UD	SA	SA	0	0			Left jugular f. almost bifurcated; spicules on sphenoid spine
2419	THINSQUARE	N	N	L/I/M	L/I/M	0	0	LN	LN	A	A	0	0			Enormous skull; spicules on sphenoid spines; thyroid cartilage ossified
2424	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged; odd spines on jugular process; thyroid cartilage ossified
2430																Missing
2432	-	N	F	-	-	-	-	-	-	-	-	0	0	-	-	Sphenoid spine growth; heavily damaged
2437	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2438	MODFLATBL	N	N	L+/I	L/I/M	+	+	UD	UD	SA	SA	0	0			Damaged; left spinosum bridged; spicules on sphenoid spines
2439	MODBLUNT	N	F	L/I	L+/I/M	+	+	LD	UD	L	L	0	0			Palatine torus; thyroid cartilage ossified
2442	MODSQUARE	N	N	L/I	L/I/M	0	0	UD	UD	L	L	0	0			Metopic suture patent; both jugular ff. almost bifurcated
2445	MODPOINT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Left jugular f. almost bifurcated, right distinctly birfurcated; heavily damaged
2449	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extremely damaged, crumbs
2458	-	-	F	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2459	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damage, dropped?; two growths at basion, small and on each side
2461	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2463	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged, crumbs
2464	DAM	N	F	L/I/M	L/I/M	0	0	UD	UD	L	L	0	0			L. pterygospinous bridge; both ff. ovales almost bridged; huge skull size
2465	BLUNT	F	F	L/I/M	L/I/M	+	+	DAM	LD	SA	SA	0	0			Spicules on sphenoid spine
2467	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Nothing but crumbs
2468	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2469	-	N	N	-	L/I/M	-	+	-	-	-	SA	0	0	-	-	Damaged
2470	-	F	B	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2471																Missing

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2472		50	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2474		63	M	VN/0	VN/0	LO	LR	M	M	M	M	0	0	0	0	0	L	L	+	+	-	-	EVEN	RD	OD
2476		63	M	-	-	-	-	-	-	-	-	0	-	-	-	-	-	-	-	+S	-	+S	-	-	RS
2477		28	F	-	-	-	LR	-	M	-	L	0	0	M	0	+	L	L	+	-	-	-	EVEN	-	-
2481		45	F	-	-	LR	LR	-	S	S	S	0	M	M	0	0	L	L	-	-	-	-	BEHIND	-	-
2483		61	M	N/0	N/0	LO	LO	L	L	L	L	0	0	0	0	0	L	L	0	0	0	0	BEHIND	RS	OS
2484		50	F	N/0	N/0	MO	MO	M	M	M	M	+	0	0	0	0	M	M	0	0	0	0	BEHIND	OS	OD
2485		76	M	DAM/0	DAM/0	LR	LR	M	M	-	M	-	-	-	-	-	L	L	0	0	-	-	-	RS	RS
2486		50	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2487		73	F	N/S0	N/0	LR	LO	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	BEHIND	RS	OS
2488		77	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2489		54	F																						
2490		86	F	-	-	-	LR	-	M	-	M	0	0	0	0	0	-	M	0	0	0	0	-	OD	OD
2493		76	F	DAM/0	DAM/0	LO	LO	M	M	S	S	0	0	0	0	0	M	M	-	-	-	-	BEHIND	-	-
2495		39	M	W/0	W/0	LO	LO	S	S	L	L	0	0	0	0	0	M	M	+S	+S	+S	+S	EVEN	RS	OD
2496		28	M	-	-	MO	SO	-	-	-	-	0	0	0	0	0	L	DAM	-	-	-	-	-	-	-
2498		53	F	W/+	W/0	LR	LR	M	M	M	M	0	0	0	0	0	S	S	0	0	0	0	EVEN	OS	OS
2500		37	F	W/0	W/0	MO	MO	L	L	M	M	0	0	0	0	0	L	L	0	0	0	+	JBEHIND	SD	SD
2501		58	M	N/0	-	MO	SO	-	-	M	M	0	0	0	0	-	S	-	0	0	-	-	EVEN	-	-
2502		70	M	-	-	MO	-	S	-	M	-	0	0	0	0	0	S	S	-	-	-	-	-	-	-
2504		66	M	-	-	-	MR	-	S	-	M	0	-	0	-	0	-	L	+	+	-	0	-	-	RD
2507		49	F	DAM/0	DAM/0	LO	LO	L	L	M	M	0	0	0	0	0	L	L	0	0	0	0	BEHIND	RD	OD
2508		82	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2510		73	F	N/0	-	MO	-	S	-	M	-	+	0	-	-	-	M	-	0	0	0	0	BEHIND	SD	SD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2472	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Nothing but crumbs
2474	MODFLATSQ	N	F	L/I	L+/I/M	++	++	BD	BD	A	A	0	0			Enormous styloid processes; thyroid cartilage ossified
2476	MODFLATBL	B	B?	-	L+/I	-	+	-	LN	-	-	0	0			Damaged; possibly dropped
2477	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged; face not present
2481	-	N	N	-	-	-	-	-	-	-	-	0	0	-	-	Damaged; face not present
2483	MODFLATBL	N	F	L+/I/M	L+/I/M	+	+	UD	UD	SA	SA	0	0			Accessory supraorbital foramen, small
2484	MODBLUNT	N	N	-	L+/I/M	+	+	BD	BD	SA	SA	0	0			Growth at basion offset to left
2485	-	B	B	-	L/I/M	-	+	-	LD	-	A	0	0		-	Basicranium damaged
2486	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged; only crumbs left
2487	MODBLUNT	F	N	L+/I	L+/I/M	++	++	LD	LD	A	A	0	0			Thyroid cartilage ossified; sphenoid spine growth; left spinosum bridged only
2488	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2489																Missing
2490	-	N	-	-	-	-	-	-	-	-	-	0	-	-	-	Face damaged/gone
2493	-	N	N	-	-	-	+	-	-	-	SA	0	0		-	Pterygobasal bridging on left, plates extend behond ovale & spinosum; small eye orbits
2495	THICKSLPOINT	N	N	0/I/M	0/I/M	0	0	BD	BD	SA	SA	0	0			Different looking face, flat; huge infraorbital foramina
2496	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2498	MODBLUNT	N	N	L/I/M	L/I/M	+	+	LN	LN	SA	SA	0	0			Right ovale almost bridged
2500	MODBLUNT	N	N	L/I/M	L/I/M	+	0	LN	LD	SA	SA	0	0			Lateral pterygoid plates very wide
2501	-	F	N	-	L/I/M	0	-	LD	-	A	-	0	0	-		Damaged
2502	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2504	MODBLUNT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2507	MODFLATBL	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged; cribra orbtalia; boney growth around f. spinosum
2508	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only part of calvarium present
2510	MODSLSQ	-	-	L+/I/M	-	0	-	-	-	A	-	-	-	-	-	Badly damaged; growth at basion offset to right

SPECIMEN		AGE		SEX		Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion		Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis		Greater palatine foramen	
			L		R	L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2511		73	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2515		69	DAM/0	M	DAM/0	LO	LO	M	L	M	L	M	M	0	0	0	0	0	0	M	M	-	-	-	-	EVEN	-	-	-
2516		32	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2518		53	W/0	F	W/0	MO	LO	L	L	L	L	M	M	0	0	0	0	0	+	M	M	0	0	0	0	BEHIND	OS	OS	OS
2519		53	W/+?	M	W/+	LR	LR	M	M	M	M	-	-	0	0	0	0	0	+	M	M	0	+	+	+	DAM	OD	OD	OD
2521		73	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
2522		46	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
2523		70	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
2524		71	DAM/+	M	DAM/0	MO	LR	M	M	M	M	M	M	+	0	0	0	0	0	L	L	0	0	0	0	EVEN	OS	OS	OS
2526		64	W/0	F	DAM/0	MO	LR	M	M	M	M	L	M	0	0	0	0	0	0	L	L	0	+	+	+	BEHIND	SD	SD	SD
2527		88	DAM/0	M	W/+	MO	MO	L	L	L	L	L	M	0	0	0	0	0	+	L	L	+S	+S	+S	+S	BEHIND	RD	RD	RD
2528		55	DAM/-	F	DAM/-	MO	-	M	-	M	S	-	S	0	-	0	0	0	-	M	M	+S	+S	+S	+S	EVEN	OS	OS	OS
2534		67	-	M	W/+	-	LR	-	M	-	M	-	M	0	-	0	+	-	-	-	L	-	-	-	-	-	-	-	-
2535		77	W/0	F	DAM/0	MO	MO	S	S	S	S	S	S	0	0	0	0	0	0	L	L	+S	+S	0	0	BEHIND	RS	RS	RS
2537		60	-	M	-	MO	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2538		81	DAM/0	M	DAM/0	MO	MR	M	M	M	M	L	M	0	0	0	0	0	0	L	L	0	0	0	-	BEHIND	-	-	OD
2540		65		F																									
2541		53	DAM/0	M	DAM/0	LO	MO	M	M	M	M	M	M	0	0	0	0	0	+	L	L	-	-	-	-	EVEN	-	-	-
2542		39	-	M	-	-	-	-	-	-	-	-	-	0	-	-	-	-	-	M	M	+	+	-	-	-	OD	OD	OD
2543		72	-	M	-	MO	-	M	M	M	M	-	M	0	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
2544		52	N/0	F	N/0	MR	MO	M	M	M	M	S	S	0	0	0	0	0	0	L	L	+S	+S	+S	+S	BEHIND	OD	OD	OD
2545		21	DAM/0	M	DAM/0	LO	LO	L	L	L	L	M	M	0	0	0	0	0	0	L	L	+	+	DAM	DAM	DAM	OS	OS	OS
2546		62		M																									
2551		65	W/0	F	DAM/0	MO	DAM	M	DAM	M	DAM	M	DAM	DAM	0	0	DAM	+	M	M	M	0	0	0	0	EVEN	OD	OD	-

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2511	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only part of calvarium present
2515	-	F	F	-	-	-	-	-	-	-	-	0	0	-	-	Basicranium broad
2516	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly damaged, crumbs
2518	MODFLPOINT	N	N	DAM	L?/I	+	+	LN	LN	SA	SA	0	0			
2519	MODBLUNT	F	N	L/I	L/I/M	0	+?	LD	LD	A	A	0	0			Extreme growth of lateral pterygoid plates; spicule growth around lesser palatine foramen
2521	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2522	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2523	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extreme damage
2524	MODFLATBL	N	N	L/I	L/I/M	0	0	LD	LD	A	A	0	0			L. jugular f. almost bridged; accessory supraorbital ff.; basion growth - 1 small left and right
2526		N	F	L/I	L/I/M	0	0	UD	DAM	SA	SA	0	0			Right spinosum bridged
2527		N	N	L/I/M	L/I/M	++	++	LD	LD	SA/L	SA/L	0	0			Right ovale bridged; large skull
2528		N	N	L+/I	L+/I	+	+	LD	LD	DAM	DAM	0	0			Damaged (dropped?)
2534	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged on left side
2535		N	F	-	L+/I	-	+	-	UN	-	SA	0	+		-	Left side of face damaged
2537	-	N	N	-	-	-	-	-	-	-	-	-	-		-	Damaged; thyroid cartilage ossified
2538		N	N	L/I/M	L/I	+	+	LD	LD	A	A	0	0			Broad face
2540																Missing
2541	-	B	B	L/I	L/I	+	+	DAM	DAM	L	L	0	0			Face damaged; spehnoid spine growth; thyroid cartilage ossified
2542	MODSLBLUNT	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2543	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2544	MODBLUNT	N	N	L/M	L/I/M	+	+	LN	LN	SA	SA	0	0			Small foramen in both supraorbital notches; blunt growth on both sphenoid spines
2545	DAM	N	F	L+/I	L+/I/M	+	++	B-	B-	SA	SA	0	0			Large growth on sphenoid spines; foramen in both supraorbital notches
2546																Missing
2551	DAM	F	N	L+/I	L+/I	+	+	LD	LD	SA	SA	0	0			Growth on sphenoid spine; left supraorbital foramen laterally offset

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2553	70	M	-	-	-	-	-	-	-	-	0	-	-	-	-	-	-	-	-	-	-	-	-	-
2554	71	M	-	-	-	-	-	-	-	-	0	-	-	-	-	M	-	-	-	-	-	-	-	-
2556	44	M	DAM	DAM	-	-	-	-	-	-	0	-	-	-	-	S	M	+	+	0	0	BEHIND	RD	RD
2557	57	F	-	-	-	MR	-	-	-	-	0	-	-	-	-	M	M	+S	-	+S	-	-	SD	-
2563	81	F	-	-	SO	-	DAM	-	-	-	-	0	-	0	-	M	-	-	-	-	-	-	-	-
2564	72	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2565	80	F	-	-	MO	-	M	-	S	S	0	0	0	0	0	-	-	-	-	-	-	EVEN	-	-
2567	52	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2568	57	F	W/0	W/0	MO	MO	M	M	M	M	0	0	0	0	0	L	L	0	0	+S	+S	BEHIND	OD	OD
2569	79	F	W/0	W/0	MO	MO	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	BEHIND	OS	OS
2570	63	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2571	67	F	-	W/?	LR	LR	M	L	M	M	0	0	0	0	0	L	L	0	0	0	0	EVEN	RD	-
2573	52	M	-	-	LO	LO	M	M	M	M	0	0	0	0	0	M	M	+	+	0	0	EVEN	OD	OD
2574	68	M	DAM/0	N/0	LO	LO	L	L	M	M	0	0	0	0	0	L	L	+S	+S	0	0	BEHIND	OD	SD
2575	68	F	N/0	N/0	LO	LO	M	M	M	S	0	0	0	0	0	M	M	+S	+S	0	0	BEHIND	OS	SS
2576	71	M	-	-	VLO	VLO	L	L	M	L	0	L	L	0	0	L	L	-	-	-	-	-	-	-
2577	48	M	DAM/0	W/0	-	LO	M	M	-	-	0	-	-	0	0	L	L	+	+	+	+	EVEN	RS	RS
2579	79	F	DAM/0	W/0	MR	MR	M	M	L	M	0	0	0	0	+	M	M	0	0	0	0	EVEN	OS	OS
2580	26	M	DAM/0	DAM/0	SO	SO	M	M	M	M	0	0	0	0	0	M	M	-	-	+S	+S	EVEN	-	RD
2581	55	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2596	70	F	W/0	-	MO	MO	M	M	M	M	0	0	0	0	0	M	M	-	-	-	-	EVEN	-	-
2602	51	M	DAM/0	DAM/0	MO	MO	M	M	-	-	-	-	-	-	-	L	L	+S	+S	+S	+S	-	RS	RS
2604	82	F	N/0	N/0	MO	MO	L	L	S	S	0	0	0	+	0	M	M	0	0	0	0	EVEN	OD	OD
2605	19	F	N/0	N/0	LR	MO	M	M	M	M	0	-	0	0	0	M	M	+S	+S	+S	+S	BEHIND	SD	SD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2553	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2554	-	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged; left supraorbital notch set very medially, w/ small foramen
2556	MODFLATBL	F	N	L/I/M	L/I/M	0	0	B?	BN	A	A	0	0			Cranium broken at all sutures
2557	MODSLSQ	N	N	-	L/I/M	-	+	-	LN	-	L?	-	-		-	Badly damaged
2563	-	N	N	-	-	-	-	-	-	-	-	0	0	-	-	Damaged; supraorbital notches almost closed into formaina
2564	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2565	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2567	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extremely damaged, crumbs
2568	MODBLUNT	N	N	L+/I	-	+	-	UN	U-	SA	-	0	0	-		Left supraorbital noth offset laterally; large spike growths on sphenoid spine
2569	THINSLBLUNT	N	N	L+/I	L+/I	+	+	UN	UN	L	L	0	0			Supraorbital notches contain small foramen
2570	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Extreme damage, almost nothing left
2571	MODSTRSQ	N	B	L/I/M	-	0	-	-	-	-	-	0	0	-	-	Face damaged; right foramen ovale almost bridged from lateral pterygoid plate
2573	MODPOINT	N	N	-	-	-	-	-	-	-	-	0	0	-	-	Face damaged
2574	MODARCHED	N	N	L/I	L/I	+	+	LN	LN	SA	SA	0	0			Metopic suture patent; thyroid cartilage ossified; foramina in supraorbital notches
2575	MODBLUNT	B	B	L/I/M	L/I/M	0	0	UN	UN	SA	SA	0	0			Some growth on sphenoid spines
2576	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Face damaged; enormous ff. ovales
2577	SLSQUARE	N	N	L+/I/M	L+/I/M	+	+	LD	LD	SA	SA	0	0			Looks similar to skulls from earlier in analysis
2579	MODSTR	F	N	L+/I	L+/I/M	+	+	LD	LD	SA	SA	0	0			Boney growth around ff. ovales and spinosa
2580	-	N	N	L/I/M	-	+	-	-	-	SA	-	0	0	-		Damaged
2581	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only part of calvarium present
2596	-	F	N	0/I/M	-	0	-	LN	-	SA	-	0	0	-		Different overall look to skull, eyes wide set; patent metopic suture
2602	DAM	N	N	L/I	L/I	0	0	UN	-	A	A	0	0	-		Growth on sphenoid spine
2604	THICKSTR	N	N	-	L/I	-	-	-	-	-	-	0	+	-	-	Supraorbital notches almost foramina and centrally located above orbits
2605	MODBLUNT	N	N	L/I/M	L/I/M	+	+	LN	LN	A	A	0	0			

SPECIMEN		AGE		SEX		Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
						L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2608		48		M		DAM/0	DAM/0	LO	LO	M	M	M	M	0	0	0	0	0	L	L	0	0	0	0	EVEN	OS	OS
2609		78		F		N/0	N/0	MO	MO	M	M	S	M	0	0	0	0	+?	M	M	+S	+S	+S	+S	EVEN	SD	SD
2610		71		M		W/0	W/0	MO	MO	M	M	M	M	0	0	0	0	0	M	M	+	+	0	0	EVEN	RS	RS
2613		46		M		N/0	N/0	MO	MO	-	M	-	-	0	-	-	-	-	M	-	+	+	0	0	EVEN	OD	OD
2622		55		M		W/0	W/0	MO	MO	M	M	L	L	0	0	0	0	0	M	M	+	+	0	0	EVEN	OD	OD
2624		35		M																							
2632		63		M		W/0	W/0	MO	LO	M	M	M	S	0	0	0	0	0	L	L	+S	+S	0	0	BEHIND	OS	OS
2634		60		M		DAM/0	DAM/0	MO	MO	M	M	S	S	0	0	0	0	0	L	L	+	+	0	++	BEHIND	OD	OD
2642		47		F		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	-	-	-	-	-
2643		63		M		N/0	N/0	MO	MO	-	M	M	M	+	0	0	0	0	L	L	0	0	0	0	EVEN	RS	RS
2647		65		F		W/0	N/0	MO	MO	S	S	M	M	0	0	0	0	0	M	M	+S	+S	+S	+S	EVEN	OD	OD
2654		61		F		W/0	W/0	MO	MR	M	M	S	S	0	0	0	0	0	L	L	0	0	0	0	EVEN	RS	SS
2661		47		M		N/0	N/0	MO	MO	L	L	M	M	0	0	0	0	0	S	S	+	+	+	+	EVEN	OD	OD
2664		47		M																							
2665		54		M		DAM/0	-	MO	-	M	-	S	-	0	0	-	0	-	M	-	-	-	-	-	-	-	-
2666		62		F		-	-	LR	LO	M	M	S	S	0	0	0	0	0	M	M	+	+S	0	-	EVEN	OD	OD
2667		30		F		W/+	W/0	MO	MO	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	BEHIND	OS	OS
2670		68		F		N/-	DAM/-	-	-	-	-	-	-	-	-	-	-	-	-	-	+S	+S	+S	+S	-	-	-
2671		56		M		W/0	W/0	LO	LO	M	-	S	S	0	L	L	0	0	L	L	+S	+S	+S	+S	EVEN	RD	RD
2675		66		M		DM/0	DAM/-	SO	-	M	-	M	M	0	0	0	0	0	L	L	+	+	+	+	EVEN	RD	RD
2676		79		M		W/0	W/0	MO	MO	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	EVEN	OS	OS
2677		12		F		W/0	W/0	MO	MO	M	M	L	L	0	0	0	0	0	L	L	0	0	0	0	BEHIND	SS	SS
2678		67		M		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2679		80		M		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2608	MODSQUARE	N	N	L++/I	L++/I	+	+	BD	BD	SA	SA	0	0			"Different looking"; thyroid cartilage ossified
2609	MODSQUARE	-	N	-	-	-	-	-	LN	-	SA	0	0		-	
2610	THICKBLUNT	N	N	L/I	L/I	+	+	LN	LN	SA	SA	0	0			Eyes set widely; spike growth on sphenoid spines
2613	MODSLBLUNT	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2622	MODPOINT	N	B	L/I	L/I/M	0	0	UN	LN	SA	SA	0	0			Huge skull; eyes set widely; ossified thyroid cartilage
2624																
2632	MODSQUARE	F	F	L/I/M	L/I/M	+	+	BD	BD	A	A	0	0			Ossified thyroid cartilage; multiple left supraorbital ff.; almost pterygospinous bridge on right
2634	MODBLUNTSQ	N	N	L/I	L/I	0	0	UN	UN	SA	SA	0	0			Very large face; triangular-shaped infraorbital foramina; "odd-looking cranium"
2642	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2643	MODBLUNT	N	B	L/I/M	L/I/M	0	0	LD	LD	SA	SA	0	0			Ossified thyroid cartilage; thick zygomas
2647	THICKSLPOINT	F	F	L/I	L+/I/M	+	+	UD	UD	L	L	0	0			Bifurcated left f. ovale, and almost bridged; gowth on sphenoid spines
2654	MODBLUNT	N	N	L++/I	L++/I/M	++	++	UN	UN	SA/L	SA/L	0	0			Growth around both ff. spinosa; both almost bridged
2661	MODBLUNT	N	N	L/M	L/I/M	+	0	LD	LD	SA	SA	0	0			Foramen in right supraorbital notch
2664																Missing
2665	-	-	-	-	-	-	-	-	-	-	-	-	-	-		Badly damaged
2666	-	F	F	L+/I	-	+	-	LD	-	-	-	0	0	-		Damaged; boney growthon both spenoid spines
2667	MODFLBLUNT	N	N	L/I/M	L/I/M	+	+	LD	LD	L	L	0	0			Posterior palate spine bifid; left f. ovale practically bridged - not quite
2670		N	N	L/I/M	L/I/M	0	0	LD	LD	L	L	0	0			Damaged; thyroid cartilage ossified
2671		N	N	L/I/M	L/I/M	+	+	LN	LN	SA	SA	+	0			Thyroid cartilage ossified
2675		N	N	L/I	L/I	0	-	LN	-	SA	-	0	0	-		Left f. spinosum bridged; small eye orbits; broad face
2676		N	N	L/I/M	L/I/M	0	0	LN	LN	SA	SA	0	0			Boad face; wide-set eyes
2677		N	N	L/M	L/M	0	0	UN	UN	L	SA	0	0			Metopic suture patent; growth on sphenoid spines
2678	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2679	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged

SPECIMEN		AGE		SEX		Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion		Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis		Greater palatine foramen	
						L	R	L	R	L	R	L	R			L	R	L	R	L	R	L	R	L	R			L	R
2680		63		F		W/-	W/-	-	-	-	-	-	-	-		-	-	-	-	L	L	0	0	0	0	-		SS	SS
2681		83		F		W/0	W/0	MO	MO	M	L	M	S	0		0	0	0	0	L	L	+	+	0	0	EVEN		RS	RS
2682		61		M		-	-	-	-	-	-	-	-	0		-	-	-	-	S	S	-	-	-	-	EVEN		-	-
2683		73		M		N/0	N/0	MO	MO	M	M	M	M	0		0	0	0	0	L	L	0	+	+	+	BEHIND		RD	RD
2688		22		M		-	-	-	-	-	-	-	-	-		-	-	-	-	-	-	-	-	-	-	-		-	-
2698		17		F		-	-	-	-	-	-	-	-	-		-	-	-	-	-	-	-	-	-	-	-		-	-
2708		37		F		W/0	W/0	MO	MO	M	M	S	S	0		0	0	0	0	M	M	+	+	0	0	EVEN		RD	SD
2710		76		F		N/0	W/+?	MR	MO	L	M	M	M	0		M	M	0	0	M	M	+	+	0	0	EVEN		OS	SS
2712		58		M		W/0	W/0	MO	MO	M	M	M	M	0		M	0	+	0	M	M	0	+	0	0	JBEHIND		OD	OD
2714		34		M		DAM/0	DAM/0	SO	-	S	-	M	-	0		0	-	0	-	S	-	+	+	-	-	EVEN		RS	OD
2717		28		F																									
2720		25		M		W/+	W/0	MO	MO	M	M	M	M	0		0	0	0	0	L	L	0	0	0	0	EVEN		OS	OS
2721		13		F		-	-	-	-	-	-	-	-	0		-	-	-	-	M	M	0	0	0	0	EVEN		OS	OS
2727		81		M		-	-	-	-	-	-	-	-	0		-	-	-	-	-	M	-	-	-	-	EVEN		-	-
2728		37		M		N/0	N/0	SO	MR	S	S	M	M	0		0	0	+	+	L	L	+S	+S	+	+S	EVEN		OD	OD
2742		66		F		N/0	N/0	LO	LO	M	M	M	M	0		0	0	+	+	M	M	+	+	+	+	JBEHIND		OD	OD
2746		85		F		W/0	W/0	LO	LR	M	L	S	S	0		0	0	0	0	L	L	0	0	0	0	BEHIND		RS	RS
2747		28		F		DAM/0	DAM/-	MR	MR	M	M	M	M	0		0	0	0	0	M	M	0	0	-	-	BEHIND		OS	OS
2748		60		F		-	-	-	-	-	-	-	-	0		-	-	-	-	-	-	+	+	+	+	-		OS	OS
2749		51		M		DAM/0	DAM/-	LR	-	M	-	M	DAM	0		0	0	+	0	M	M	0	0	-	-	EVEN		-	-
2750		53		F		W/0	W/0	MO	MO	M	M	M	S	0		0	0	+	+	L	L	+S	+S	0	0	BEHIND		OS	OS
2751		71		F		W/0	W/0	MO	MO	M	M	M	M	0		0	0	0	0	L	L	+S	+S	+S	+S	EVEN		SD	SD
2752		17		F		W/0	W/0	MO	MO	M	M	S	S	0		0	0	0	0	M	M	0	0	+S	+S	BEHIND		OS	OS
2753		66		M		W/-	W/-	-	-	-	-	-	-	-		-	-	-	-	L	L	0	0	0	0	-		SS	SS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2680																Missing
2681	MODSLBLUNT	N	N	L/I	L/I	0	0	LN	-	SA	-	0	0	-		Short blunt growth on right sphenoid spine
2682	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2683	MODSTBLUNT	N	N	L/I	L/I/M	0	0	LD	LD	SA	SA	0	0			Left jugular f. almost bifurcated
2688	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly damaged
2698	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly damaged
2708	MODSLBLUNT	F	F	L/I/M	L/M	++	+	LN	LN	SA	SA	0	0			Growth on spenoid spines
2710	MODSQUARE	B	F	L/I/M	L/I/M	0	0	UD	UD	L	L	0	0			Pterygospinous bridge almost complete on right; different looking face, supraorbital ridges
2712	MODBLUNT	N	N	L/I/M	L/I/M	0	0	UD	UD	L	L	0	0			Huge greater palatine foramen; huge face
2714	-	N	N	L/I	L/I/M	0	0	DAM	-	SA	SA	0	0	-		
2717																Missing
2720	MODSLBLUNT	N	N	O/I	O/I	0	0	LN	LN	SA	SA	0	0			Pterygobasal bridging on right; small foramina in supraorbital notches
2721	-	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2727	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2728	MODSLSQ	N	N	L/I	L/I/M	+	+	BD	BD	SA	SA	0	0			Pterygospinous bridge almost complete on left; ossified thyroid cartilage
2742	THICKSLBLNT	N	N	L/I/M	L/I/M	0?	0?	DAM	DAM	SA	SA	0	0			Slightly damaged; right jugular foramen bifurcated mediolaterally
2746	THICKSLPOINT	N	F	L/M	L/M	0	0	UN	UN	L	L	0	0			Right supraorbital foramen set laterally; left infraorbital foramen bifurcated/doubled
2747	MODSQUARE	N	N	L/I/M	L/I/M	0	0	DAM	UN	L	L	0	0			Foramina in supraorbital notches; very round eyes
2748	MOD/DAM	N	B	-	L/M	-	-	-	+	-	-	0	0		-	Foramen in left supraorbital notch; cribra orbitalia; damaged - dropped?
2749	-	N	N	L/I/M	L/I/M	+	+	UN	UN	SA	SA	0	0			
2750	MODSQUARE	N	N	L/I/M	L/I/M	++	++	UD	UD	SA	SA	0	0			
2751	MODSLSTR	N	N	L+/I/M	L/I/M	+	+	UN	UN	SA	SA	0	0			Growth on sphenoid spines around the ff. spinosa
2752	MODSLSQ	B	B	L/I/M	L/I/M	+	+	LN	LN	L	L	0	0			Left pterygoid plate partially bridging to sphenoid spine
2753	THICKSQUARE	F	F	L/I/M	L+/I/M	++	++	LD	LD	SA	SA	0	0			Dess. flesh obscuring base; l. infraorb. f. double; ossified thyroid cart.; huge abcess @ incisive f.

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2755		16	F	-	-	-	-	-	-	-	-	0	0	0	-	0	S	S	0	0	+S	+S	-	RD	RD
2764		90	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2776		84	F	-	-	-	-	-	-	-	-	-	-	-	-	-	S	S	S	0	-	-	-	-	SS
2782		53	M	-	-	MO	MO	-	-	S	S	0	-	-	0	0	DAM	M	-	-	-	-	JBEHIND	-	-
2784		70	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2787		77	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2789		65	F	W/0	W/0	MO	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	BEHIND	OS	OS
2799		27	M	-	-	MO	-	S	-	-	-	-	-	-	-	-	M	-	+S	-	-	-	-	RD	-
2801		79	M	-/0	-/0	MO	MO	S	S	-	-	0	0	0	0	-	DAM	L	0	0	0	0	-	OD	RS
2802		45	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2803		73	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2804		78	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2808		60	M	-	-	-	-	-	-	-	-	0	-	-	-	-	S	S	-	-	-	-	-	-	-
2809		41	F	W/0	W/0	MO	MO	M	L	S	S	0	0	0	0	0	M	M	0	0	+S	+S	BEHIND	SS	SS
2811		50	M	N/0	N/0	LO	LO	L	L	M	M	0	L	L	0	0	M	M	+S	+S	0	0	JBEHIND	OD	OD
2812		71	M	N/0	N/0	MO	LO	M	M	M	M	0	0	0	0	0	M	M	+	+	0	0	JBEHIND	OD	OD
2817		56	F	N/0	N/0	MO	MO	M	M	M	M	0	0	0	0	+	M	M	0	0	0	0	BEHIND	OD	OD
2818		71	M	DAM/0	W/0	LO	LO	M	M	L	L	0	0	0	0	0	L	L	-	+	-	-	EVEN	-	RD
2822		59	F	W/0	W/0	MO	MO	M	M	S	S	0	L	L	0	0	M	M	0	0	0	0	BEHIND	OS	OS
2829		74	M	W/0	W/0	LO	LO	L	L	M	M	0	0	0	0	0	M	M	0	0	0	0	JBEHIND	OS	OS
2843		28	F	W/0	W/0	MO	MO	L	L	L	L	0	0	0	0	0	L	L	+S	+S	0	0	BEHIND	OS	OS
2847		66	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2849		76	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2850		47	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2755	MODSLPOINT	B	B	L/I/M	L/I/M	0	0	LD	LD	-	-	0	0			
2764																Missing
2776	-	F	F/B?	-	O/I	-	++	-	UN	-	-	0	0		-	Damaged - dropped?
2782	-	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2784																Missing
2787	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2789	THINSLSQ	N	N	L/I	L/I	0	0	LD	LD	L	L	0	0			Basicranium damaged; ossified thyroid cartilage
2799	-	N	-	-	-	-	-	-	-	-	-	-	-		-	Damaged - dropped?; foramen in left supraorbital notch
2801	THINSTRSQ	F	N	L/I/M	L/I/M	0	0	LD	LD	A	A	0	0			Flat, broad face; frowth on sphenoid spine; significant alveolar repsorption
2802	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only small fragments are present
2803	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2804	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2808	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only part of skull present; thyroid cartilage ossified
2809	MODSLPOINT	N	N	L/M	L/I/M	0	0	UD	UD	A	A	0	0			Spiked growth on sphenoid spines; left f. ovale bifurcated
2811	THICKSTRSQ	F	F	L+/I	L/I/M	0?	0?	LD	LD	SA	A	0	0			Wide face; part of thyroid cartilage ossified
2812	MODSLBLUNT	N	N	L/I	L/I	0	0	LD	BD	SA	SA	0	0			Narrow face; large blunt growths on sphenoid spines
2817	MODSLPOINT	N	N	L/I/M	L/I/M	+	+	LD	LD	L	L	0	0			Thyroid cartilage ossified; metopic suture patent; multiple infraorbital ff.; ff. in supraorbital notches
2818	-	-	N	-	L/M	-	+	-	LD	SA	SA	-	0		-	Damaged - dropped?; left f. ovale bifurcated; right ovale almost bridged
2822	THINSLBLUNT	N	N	L/I	L/I	+	+	UN	UN	SA	SA	0	0			Foramina in supraorbital notches
2829	THICKSLBLNT	N	N	L+/I	L+/I	+	+	BD	BD	A	A	0	0			Blunt growth on sphenoid spine; ff. in supraorbital notches; huge infraorbital ff.; rectangular orbits
2843	THINSLPOINT	N	N	L/I/M	L/I/M	0	0	UN	UN	SA	SA	0	0			Foramina in supraorbital notches
2847	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
2849	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
2850	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2856	52	M	DAM/0	-	MR	-	-	-	-	-	-	-	-	-	-	-	-	+	+	0	0	-	OD	SD
2857	68	M	-/0	-/0	MO	MR	L	L	M	M	0	0	0	0	+	M	M	-	-	-	-	EVEN	-	-
2860	52	F	W/0	W/0	MO	MO	M	M	M	S	0	0	0	0	0	M	M	0	0	0	0	BEHIND	SS	OS
2861	76	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2863	63	M	-	-	-	-	-	-	-	-	0	?	?	0	0	S	S	-	-	-	-	-	-	-
2867	61	F	-	-	MO	MO	M	M	S	S	0	0	0	0	0	L	L	-	-	-	-	EVEN	-	-
2872	27	F	W/+	W/+	MO	MO	L	L	M	M	0	0	0	0	0	M	M	0	0	0	0	EVEN	OS	OS
2875	38	M	-	-	-	-	-	-	-	-	0	-	0	-	0	-	-	0	0	0	0	EVEN	OS	OS
2882	53	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2884	32	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2885	47	F	DAM/0	DAM/0	MR	MO	M	M	S	M	+	0	0	0	0	L	L	+S	+S	0	0	BEHIND	OS	OS
2889	70	F	-/0	-/0	MO	MO	M	M	S	S	0	0	0	0	0	L	L	-	-	-	-	BEHIND	-	-
2891	41	F																						
2893	38	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2898	77	M	N/0	VN/0	MO	MO	S	S	S	M	0	0	0	0	0	-	L	+S	+S	0	0	EVEN	OS	OS
2899	31	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2902	46	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2903	18	M	W/0	W/0	MO	MO	M	M	M	M	0	0	0	0	+	M	L	0	0	0	0	EVEN	OS	OS
2909	49	M	-/0	-/0	MO	LO	M	L	-	L	0	0	0	-	0	M	M	0	0	0	0	-	OS	OS
2910	57	M	W/+	W/0	MO	MO	M	M	M	M	0	0	0	0	0	S	S	+S	+S	+S	+S	BEHIND	RS	RD
2913	75	M	DAM/0	DAM/0	LO	LR	M	M	L	L	0	0	0	0	0	L	L	0	0	0	0	EVEN	RS	RS
2916	64	?																						
2917	69	M	W/0	W/0	MO	MO	L	L	M	M	0	0	0	0	0	M	M	+S	+S	+S	+S	EVEN	OD	OD
2918	57	F	W/+	W/0	LR	MO	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	EVEN	SD	SD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2856	MODSLBLUNT	N	N	L/I/M	L/I/M	+	+	LD	DAM	SA	SA	0	0			Damaged
2857	-	F	F	-	-	-	-	-	-	-	-	0	0	-	-	Metopism; left infraorbital foramen three openings - not accessory foramen
2860	MODSLBLUNT	F	F	L/I/M	L/I/M	+	+	BD	BD	A	A	0	0			Supraorbital foramen located centrally above orbits
2861	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2863	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged; odd spikes on jugular processes
2867	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2872	THINSLPOINT	F	N	L+/I/M	L+/I/M	+	+	UD	UD	SA	SA	0	+			Left infraorbital foramen opens anterolaterally
2875	THICK/DAM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2882	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2884	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged, only crumbs left
2885	MODBLUNT	N	N	L/I/M	L/I/M	0	DAM	LN	-	A	A	-	-	-		
2889	-	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Face badly damaged; foramen in supraorbital notches
2891																Missing
2893	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2898	MODPOINT	N	F	L/I	L/I	0	0	BD	BD	SA	SA	0	0			Thyroid cartilage ossified; foramen in left supraorbital notch
2899	-	N	N	L/I	L/I/M	+	+	LN	LN	SA	SA	0	-			Basicranium damaged
2902	-	F	F	-	L/I/M	-	+	-	-	-	A	-	0		-	Left side and base damaged
2903	THICKSLSQ	N	N	L/I/M	L/I/M	+	+	BD	BD	SA	SA	0	0			Very large greater palatine foramina
2909	MODSTBLUNT	-	-	L/M	-	-	-	-	-	-	-	-	-	-		Damaged - dropped?
2910	MODBLUNT	N	N	L+/I/M	L+/I/M	+	+	LD	LD	SA	SA	0	0			Metopic suture patent; r. ovale almost bridged; foramen in supraorbital notches; gold dentures
2913	MODBLUNT	N	N	L+/I/M	L+/I/M	+	+	LD	LD	SA	SA	0	0			
2916																Missing
2917	MODBLUNT	N	F	L+/I/M	L+/I/M	0	0	LD	LD	A	A	0	0			Thyroid cartilage ossified; tall orbits; pterygospinous bridging almost complete on right
2918	MODSLPOINT	F	F	L/I/M	L/I/M	0	0	LN	LN	L	L	0	0			Pterygobasal bridging, straight spicule

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bridged		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenoocciptal synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
2920		74	F	N/0	N/0	MO	MO	M	M	M	M	0	0	0	+	+	S	S	0	0	0	0	EVEN	SD	SD
2921		38	F	N/0		MO		M		M		0	0	0	+		S		0	0	0	0	EVEN	SD	
2926		60	M	W/+	-/+	LR	-	M	-	M	L	0	0	0	0	+	S	S	0	-	0	-	EVEN	RD	-
2927		76	M	W/0	W/0	LO	LO	L	L	S	S	0	0	0	0	0	S	S	0	0	0	0	EVEN	OD	OD
2930		35	F	W/0	W/0	MO	MO	M	M	S	S	0	-	-	0	-	S	S	+S	0	0	0	EVEN	OS	OS
2936		75	M	-/0	-/-	MO	-	L	-	-	-	-	0	-	+	-	M	-	-	-	-	-	-	-	-
2939		35	M	-/-	-/0	-	LO	-	M	-	M	-	-	0	-	0	-	L	-	+	-	0	-	-'	RD
2943		70	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2948		57	M	-/0	-/0	LO	LO	M	M	M	M	0	0	0	0	0	M	-	-	-	-	-	-	-	-
2949		45	F																						
2954		32	F																						
2955		69	M																						
2956		43	M	W/0	W/0	MO	MO	L	L	S	S	0	0	0	0	0	L	L	+	+	0	0	BEHIND	RS	OS
2957		39	F	N/0	N/0	MO	MO	L	L	S	S	0	0	0	0	0	M	M	0	0	0	0	EVEN	SS	SS
2960		37	?	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2963		69	M	W/0	W/0	MO	MO	M	M	M	M	0	0	0	0	0	M	M	+S	+S	+S	+S	JBEHIND	RS	OS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
2920	MODSLPOINT	B	N	L/I/M	L/I/M	0	0	LD	LD	SA	SA	0	0			Slight bulges at infraorbital angles
2921																Missing
2926	-	N	N	-	-	0	-	LN	-	L	-	0	0	-		Pterygobasal bridging on both sides
2927	THICKSLSQ	N	N	L/I	L/I	0	0	UD	UD	SA	SA	0	0			Thyroid cartilage ossified; accessory supraorb. ff. huge infraorb. ff.; blunt growth on shpenoid
2930	MODSLPOINT	N	F	L/I/M	-	+	0	UN	-	SA	-	+	+	-		
2936	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Blunt growth on sphenoid spine; badly damaged
2939	DAM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
2943	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2948	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
2949																Missing
2954																Missing
2955																Missing
2956	MODSLPOINT	N	N	L/I/M	L/I/M	+	+	LN	LN	SA	SA	+	+			Blunt growth on sphenoid spine; foramina in supraorbital notches
2957	MODSLPOINT	B	N	L/I/M	L/I/M	0	0	UD	-	SA	SA	0	0			Only part of parietal present
2960	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Large bridging spur on both lateral pterygoid plates
2963	THINBLUNT	N	N	L/I/M	L/I/M	+	+	UD	UD	SA	SA	0	0			Thyroid cartilage ossified

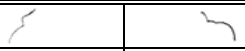
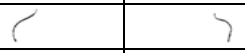
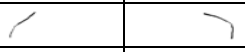
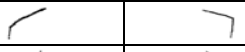
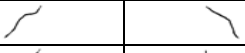
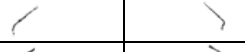
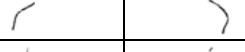
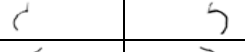
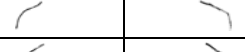
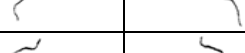
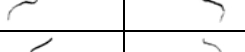
APPENDIX B

COMPARATIVE DATA COLLECTED FROM THE TERRY COLLECTION SAMPLE

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenoocciptal synchondrosis	Greater palatine foramen	
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
871	56	M	N/0	N/0	MO	MO	M	M	M	M	0	M	M	0	0	L	L	+	+	+	+	JBEYOND	OD	OD
867	38	M	N/0	N/0	LO	LO	M	M	M	M	0	M	M	+	+	M	M	+	+	+S	+S	BEHIND	RD	OD
810	54	M	N/0	N/0	LR	MO	S	M	L	L	0	0	0	0	0	M	M	+	+	++	++	EVEN	RD	RD
802	36	M	N/0	N/0	LO	MO	L	L	S	S	0	0	0	0	0	L	L	+	+	+S	+S	BEHIND	RD	RD
763	46	M	N/0	N/0	LO	LO	M	M	M	M	0	0	0	0	0	L	L	+	+	+	+	BEHIND	RD	RD
557	46	M	DAM/0	W/0	MO	MO	S	S	L	L	0	0	0	0	0	L+	L+	+	+	+	+	EVEN	OD	?D
778	55	M	N/0	N/0	LO	LO	M	M	L	L	0	0	0	+	0	L	L	0	0	0	0	BEHIND	OD	OD
772	56	M	N/0	N/0	MO	MO	?	M	M	M	0	M	M	0	0	L	L	0	0	0	0	BEYOND	OD	OD
918	40	M	N/0	N/0	MO	LO	M	M	M	M	0	0	0	0	0	L	L	0	0	0	0	EVEN	RS	RS
924	43	M	VN/0	VN/0	LO	LO	L	L	L	DAM	0	M	M	0	0	M	M	+	+	+	+	EVEN	OD	OD
866	60	M	N/0	N/0	MR	MR	M	M	S	S	0	M	M	0	0	L	L	+S	+S	+S	+S	EVEN	OD	OD
762	59	M	W/0	W/0	LO	LO	M	M	S	S	0	M	M	0	0	L	L	0	0	+	+	EVEN	OD	OD
1023	20	M	W/0	W/0	MO	MO	L	L	M	M	0	0	0	0	+	M	M	0	0	+	+	BEHIND	SD	SD
872	48	M	W/0	N/0	LO	LO	M	M	M	M	0	M	M	+	+	M	M	DAM	+S	+	+	BEHIND	RS	RS
879	50	M	W/0	W/0	LO	LO	M	M	M	M	0	M	M	0	+	L	L	+	+	+	+	BEHIND	RD	RD
898	22	M	M/0	M/0	MO	MO	M	M	S	S	0	0	0	0	0	M	M	+	+	+	+	EVEN	OD	OD
707	26	M	N/0	N/0	LO	LR	S	S	S	S	0	0	0	+	+	M	M	+	+	+	+	JBEYOND	SD	SD
830	28	M	N/0	N/0	LO	LO	L	S	S	S	0	0	0	0	0	DAM	M	+	+	+S	+S	BEYOND	SD	SD
619	31	M	N/0	N/0	LO	LO	S	S	S	S	0	0	0	0	0	L	L	+	+	0	0	BEYOND	OD	OD
882	35	M	W/0	W/0	MO	MO	S	S	S	S	0	0	0	0	0	M	M	++	++	+S	+S	JBEYOND	SD	SD
836	36	M	W/0	W/0	LO	LR	M	M	S	S	0	0	0	0	0	M	M	0	0	0	0	JBEYOND	SS	RS
799	38	M	W/0	W/0	LR	LR	M	M	S	S	0	M	M	0	0	L	L	+S	+S	+	+	BEYOND	OS	OS
933R	40	M	W/~	W/0	LR	LR	M	S	S	S	0	0	0	0	0	L	L	+	+	+	+	JBEYOND	OD	OD
663	44	M	N/0	N/0	LR	LO	S	M	S	S	0	M	M	0	0	L	L	+	+	+	+	BEHIND	OD	OD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
871	THICKSQPOINT	N	F	L/I/M	L/I/M	+	+	UD	UD	A	A	0	0			Postglenoid plate very large; palatine torus
867	THINROUND	N	N	L/I/M	L/I/M	0	0	BD	BD	A	A	0	0			Deveiated septum
810	THICKBLUNT	N	N	L/M	L/M	+	+	LD	LD	SA	SA	0	0			Growth from between
802	MODPOINT	F	BOTH	L/M	L/M	+S	0	BN	BN	A	A	0	0			Supraorbital foramina may be frontal formaina; Boney spur almost covers left f. spinosum
763	THICKPOINT	F	N	L/I/M	L/I/M	+S	+S	LN	LN	SA	SA	0	0			Boney spurs around left f. spinosum
557	DAM	N	N	0/I/M	0/I/M	+S	+S	BN	BN	SA	SA	0	0			
778	STRBLUNT	N	N	L/I/M	L/I/M	+S	+S	UD	UD	SA	SA	0	0			Left jugular foramen very constricted/small; no lesser palatine foramina present
772	THINBLUNT	N	N	L/I/M	L/I/M	+	+	LN	BN	A	A	+VS	0			Left ovale and spinosum connected; infraorbital foramina round and deep
918	FLAT	BOTH	2F	L/I/M	L/I/M	+	+	UN	UN	SA	SA	0	0			Foramen of Huscke on right; right f. spinosum at tip of spine
924	FLAT	BOTH	BOTH	L/I/M	L/I/M	+S	+S	LN	LN	SA	SA	0	0			
866	THCKSQUARE	N	N	L/I/M	L/I/M	0	0	BD	BD	SA	SA	0	0			
762	MODPOINT	N	N	2L/I/2M	2L/I/2M	0	0	LN	LN	SA	SA	0	0			2 infraorbital foramina on each side; odd indentation on frontal
1023	THICKPOINT	F	N	L/I/M	L/I/M	+	+	UN	UN	SA	SA	0	0			
872	MODROUNDBL	N	N	L/I/M	L/I/M	0	0	UD	UD	SA	SA	0	0			
879	MODPOINT	2F	BOTH	L/I/M	L/I/M	+	+	BD	BD	A	A	0	0			R. formaen spinosum bridged w/ loop of bone
898	THICKROUND	F	N	2L/2I/M	2L/2I/M	0	0	BN	BN	A	A	0	+			Ff. ovales and spinosa close together
707	THICKROUND	N	N	L++/I	L++/I	0	0	UN	UN	A	A	+	0			Ff. ovales and spinosa very close together; R. jugular f. bridged close to condyle
830	THICKPOINT	N	N	L/I/M	L/I/M	0	0	BN	BN	A	A	+	+			
619	THICKBLUNT	N	N	L/I	L/I	+	+	LN	LN	A	A	0	0			
882	THICKROUND	F	F	L/I/M	L/I/M	+	+	UN	UN	A	A	+	0			Left f. ovale almost brisged by boney spur; odd spur growth on petrosal
836	THICKSQUARE	N	N	L/I/M	L/I/M	+	0	LN	LN	SA	SA	0	0			
799	THICKROUND	2F	BOTH	L++/I/M	L++/I/M	0	0	LN	LN	A	A	0	0			Left f. ovale not complete; right f. spinosum opens into right f. ovale
933R	THICKPOINT	N	N	L/I/M	L/I/M	0	0	BN	BN	A	A	0	0			R. pterygospinous bridging almost complete; left f. ovale bridged; small ff. on supracillary arches
663	MODSLPOINT	BOTH	BOTH	L/M	L/M	0	0	BN	BN	A	A	0	0			L. f. ovale brdiged; supraorbital formaina placed very laterally

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenoocciptal synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
923		46	M	N/0	W/0	MO	MO	L	M	M	M	0	0	0	0	0	M	M	+	+	+	+	EVEN	RS	RS
875		50	M	N/0	N/0	LO	LR	M	M	S	S	0	M	M	0	0	DAM	L	0	+	+	+	EVEN	OS	OS
811		51	M	N/0	N/0	MR	LR	M	S	M	S	0	0	0	+	0	L	L	+	+	+S	+S	EVEN	OS	RS
816		54	M	W/0	W/0	LO	LO	M	M	S	S	0	0	0	0	0	L	M	+	+	+S	+S	BEHIND	SS	SS
986		65	M	N/0	N/0	LO	LO	M	M	S	S	0	M	M	0	0	M	M	+	+	+S	+S	BEYOND	OS	OS
990		28	M	N/0	N/0	LO	LO	M	M	S	S	0	0	0	0	0	M	M	+S	+S	+S	+S	BEHIND	RD	RD
880		27	F	W/+	W/0	LO	MO	S	S	L	M	0	L	L	+	0	L+	L+	0	0	0	0	BEHIND	RS	RS
745R		34	F	W/0	W/0	LO	MO	M	M	M	M	0	M	M	0	0	S	DAM	0	0	+S	+S	EVEN	SD	SD
1186		44	F	W/0	W/0	MR	MR	S	S	M	L	0	L	L	0	0	M	M	0	0	+	+S	EVEN	SD	SD
928R		44	F	W/0	W/+	MR	MR	S	S	M	M	0	M	M	0	0	M	M	+S	+S	0	0	BEHIND	OS	OS
1239R		52	F	N/0	N/0	SO	DAM	S	DAM	S	S	0	0	0	0	0	DAM	DAM	0	0	+S	0	EVEN	RD	OD
1174		53	F	W/0	W/0	MR	MR	M	M	M	L	0	L+	M	0	0	M	M	0	0	+	+	BEHIND	OD	RD
554R		55	F	M/0	M/+	LR	LO	M	M	M	DAM	0	0	0	0	0	L	L	+	+	+	+	BEHIND	SD	SD
1094		57	F	W/+	W/+	MO	MO	M	M	M	M	0	M	M	+	+	S	S	0	0	+	+	EVEN	OD	OD
934		62	F	M/0	M/0	MR	MO	-	S	M	M	0	0	0	0	0	L	L	0	0	+S	+S	EVEN	SS	SS
869		59	F	M/0	M/0	MO	MO	M	S	S	S	0	0	0	+	0	L	DAM	0	0	+S	+S	EVEN	OD	OD
1153		30	F	M/0	M/0	LR	LR	M	S	M	M	0	M	M	0	0	M	M	0	0	+S	+S	EVEN	OD	OD
405R		35	F	M/0	M/0	MR	MR	M	S	L	L	0	M	M	0	0	M	M	+	+	+	+	EVEN	SS	SS
135R		30	F	W/0	W/0	MR	MO	M	M	M	M	0	M	M	+	0	L	L	+	+	+S	+S	EVEN	OS	OS
710R		60	F	W/0	W/0	MO	SO	M	M	M	M	0	0	0	0	0	M	M	+S	+S	+S	+S	BEYOND	SD	SD
925		71	F	M/0	M/0	SR	MR	M	S	L	L	0	M	M	0	0	L	L	+	+	+S	+S	EVEN	SD	SD
970		21	F	M/0	M/0	MO	MO	M	M	S	S	0	S	S	0	0	M	M	+	+	0	0	BEYOND	OD	OD
926		23	F	M/0	M/0	LO	LO	M	M	S	S	0	S	S	0	0	M	M	+	+	0	0	EVEN	SD	SD
887		34	F	N/0	N/0	MO	MO	M	M	S	S	0	S	S	0	0	DAM	DAM	0	0	+S	+S	EVEN	SS	SS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
923	MODROUND	N	N	L/M	L/M	0	0	BN	BN	A	A	0	0			Right f. spinosum placed at tip of spine
875	MODSQUARE	N	N	2L/I/M	L/I/M	0	0	BN	BN	A	A	0	0			Two infraorbital formaina on left
811	THICKSLPOINT	BOTH	BOTH	L/I/M	L/I/M	0	0	LN	LN	A	A	0	0			Right frontal f. placed very latrerally; left supraorbital f. medially placed
816	THINBLUNT	N	N	L/M	L/I/M	0	0	LD	LD	A	A	0	0			R. f. spinosum has a thin slip of a bridge - from small spur
986	THICKBLUNT	N	BOTH	L/I/M	L/I/M	0	0	LN	LN	A	A	0	0			Two small infraorbital foramen on right
990	THICKSQUARE	N	N	L/I	L/I/M	0	0	LN	LN	SA	SA	0	0			Latral pterygoind plates flared widely
880	THICKSQUARE	N	N	L/M	L+/M	+	+	UN	UN	SA	SA	0	0			Inferior border of orbits round in shape
745R	MODSQUARE	N	F	L/I/M	L/M	0	0	LN	LN	SA	SA	0	0			
1186	MODSQUARE	F	N	L/M	L/M	0	0	UN	UN	SA	SA	0	0			
928R	MODPOINT	N	N	L/I/M	L/I	0	0	UN	UN	SA	SA	0	0			
1239R	THICKROUND	N	N	L/I/M	L/I/M	0	0	LN	LN	SA	SA	0	0			
1174	THICKBLUNT	2N	1F	2L+/I/M	2L/I/M	+	+	LN	LN	SA	SA	0	0			Left f. spinosum bridged, right almost; two infrorbital foramina on each side
554R	THINPOINT	N	F	L/I/M	L/I/M	0	0	UN	UN	SA	SA	0	0			
1094	THICKBIFID	N	N	L/M	L/M	0	0	UN	UN	SA	SA	0	0			Pterygospinous bridging evident; cribra orbitalia
934	THICKBLUNT	F	BOTH	L/I	L/I	0	0	LN	LN	L	L	0	0			R. frontal f. laterally placed; left f. spinosum opens into f. ovale
869	THICKSQUARE	N	N	L/I+	L/I+	0	0	UN	UN	A	A	0	0			Lateral pterygoid plate flared, but not wide
1153	THICKBLUNT	N	N	L/I/M	L/I/M	0	0	LN	LN	SA	SA	0	0			Formaina in supraorbital notches
405R	THICKBLUNT	N	N	L++/I/M	L++/I/M	++	++	LN	LN	SA	SA	0	0			F. ovale bifurcated
135R	MODSQUARE	BOTH	BOTH	L+/I/M	L/I/M	+	+	UN	UN	SA	SA	0	0			
710R	THICKPOINT	BOTH	BOTH	L++/I	L++/I	++	++	LN	LN	SA	SA	0	0			
925	THICKBLUNT	F	F	L/I/M	L/I/M	+S	+S	UD	UD	SA	SA	0	0			
970	THICKBLUNT	N	N	L/I/M	L/I/M	0	0	BN	BN	SA	SA	0	0			
926	MODBLUNT	N	F	L+/I/M	L+/I/M	+	+	BN	BN	A	A	0	0			
887	THICKDBLEBL	F	F	L/M	L/M	0	0	BN	BN	A	A	0	0			

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
927		35	F	N/0	N/0	LO	LO	M	M	S	S	0	S	S	0	0	M	M	+	+	0	0	EVEN	SS	SS
921		38	F	N/0	N/0	MO	LO	S	M	M	M	0	S	S	0	0	M	M	+	+	0	0	EVEN	OD	OD
913		27	F	N/0	N/0	LR	LR	M	L	M	M	0	S	S	0	0	S	S	+	+	+	+	EVEN	OD	OD
625R		39	F	M/0	M/0	LO	LO	M	L	S	S	0	M	M	0	0	L	DAM	+	+	0	0	EVEN	SS	SS
988		40	F	W/0	W/0	LO	LO	M	M	S	S	0	S	S	0	0	L	L	+	+	+	+	BEYOND	SD	SD
658R		44	F	VN/0	VN/0	LR	LR	S	L	S	S	0	M	M	0	0	DAM	L	+	+	0	0	BEYOND	OS	OS
1021		48	F	M/0	M/0	LO	LO	M	S	M	M	0	S	S	0	0	M	M	+	+	+	+	EVEN	OD	OD
873R		48	F	N/0	N/0	MO	MO	M	L	S	S	0	S	S	0	0	M	M	+	+	+S	+S	EVEN	OD	OD
603		50	F	W/0	W/0	MO	MO	S	S	S	S	0	M	M	0	0	M	M	+	+	+	+	BEHIND	OS	OS
1083		40	F	M/0	M/0	MO	LO	M	S	S	S	0	M	M	0	0	L	L	+	+	+	+	EVEN	SD	SD
815		32	F	N/0	N/0	SO	MO	M	M	M	M	0	M	M	0	0	L	L	+	+	0	0	EVEN	OS	OS
766		35	F	W/0	W/0	MO	MO	M	M	S	S	0	S	S	0	0	L	L	+	+	+	+	EVEN	RD	RD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
927	THICKSQUARE	N	N	0/I/M	0/I/M	0	0	BN	BN	SA	A	0	0			Os japanicum
921	DAM	N	N	L+/I/M	L+/I/M	+	+	BN	BN	A	A	0	0			
913	THICKPOINT	N	F	L/I	L+/I/M	+	+	BN	BN	A	A	0	0			Right ff. ovale and spinosum, and left f. open into respective fissures
625R	THICKSQUARE	N	N	L/I	L/I/M	0	0	BN	BN	A	A	0	0			
988	MODSQUARE	BOTH	BOTH	L++/I	L++/I	++	++	LN	LN	A	A	0	0			Left infraorbital foramen and supraorbital formaina very laterally placed
658R	THICKSQUARE	N	N	L/I/M	L/IM	+S	+S	BN	BN	SA	SA	0	0			
1021	THICKBLUNT	F	F	L/I/M	L/I/M	+	+	BN	BN	SA	SA	0	0			two supranumerary ff. on zygomatic process of frontal bone
873R	MODSQUARE	N	N	L++/I	L+/I/M	++	++	BN	BN	L	L	0	0			Vomer/septum missing
603	THICKBLUNT	N	N	L/i+	L/I+	+S	+S	BN	BN	L	L	0	0			
1083	VTHICKBLUNT	F	N	L+/I	L+/I/M	+	+	BN	BN	SA	SA	0	0			
815	THICKBLUNT	BOTH	BOTH	L+/I	L+/I/M	0	0	BN	BN	SA	SA	0	0			Infraorbital foramina very small
766	THICKSQUARE	N	N	L/I/M	L/I/M	0	0	LN	LN	SA/L	SA/L	0	0			Pterygospinous bridging on right almost complete

APPENDIX C

COMPARATIVE DATA COLLECTED FROM THE CAMPBELL FARM SITE SAMPLE

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen		Palate shape
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R	
1/105	A	F	-	-	LO	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3/107	A		-	-0	-	LO	-	M	-	-	0	-	-	-	-	L	L	-	-	-	-	-	-	-	-
3/220	A	F	-	-	LO	-	L	-	M	M	0	0	0	0	0	M	M	-	-	-	-	VBEHIND	SD	-	-
5/391	A	-	-	-	MR	MR	M	M	-	-	0	-	-	-	-	L	L	+	+	+	+	-	OD	OD	-
6/243	A		-/+	-	MO	MR	-	L	-	-	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
7/244	A	F	-	-	-	SR	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
11/242	A	M	-	-	-	MO	-	-	-	-	-	-	-	-	-	M	M	0	0	0	0	-	OS	OD	-
22/533																									
23/558																									
32/732																									
39/714																									
40/885	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
41/744	A	M	N/0	N/0	MR	MR	M	M	VS	VS	0	-	-	0	0	L	L	0	0	0	0	-	OD	OD	-
42/779			-/0	-	-	MO	-	L	-	-	0	-	-	-	0	M	M	-	-	-	-	-	-	-	-
47/1158	A	M	-	-	-	-	M	-	M	M	0	-	0	0	+	M	M	-	+S	-	+S	BEHIND	-	OD	-
48/1047	A	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53/1194																									
59/1225	A	M	-	-	LO	LO	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
62/1297	A	M	-/+	-/0	LR	LR	L	M	-	-	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
64/1422	A	F	-	-	MR	-	L	-	-	-	-	-	-	-	-	M	-	-	-	-	-	-	-	-	-
70/1476																									
71/1475	A	F?	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
72/1483	-	-	-	-	MR	MR	-	M	-	-	-	-	-	-	-	M	L	-	-	-	-	-	-	-	-
79/1607																									
80/1628	AD	F	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-

SPECIMEN	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
	L	R	L	R	L	R	L	R	L	R	L	R	R	L	
1/105	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
3/107	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
3/220	F	F	-	-	-	-	-	LN	SA	-	-	-		-	Foramina of Hushke preset bilaterally
5/391	F	F	L/I/M	L/I/M	0	0	LN	-	SA	-	-	-		-	Foramen ovales and spinosa very close together
6/243	F	F	-	-	-	-	-	-	-	-	-	-	-	-	Pterygospinous bridginbg on right, but lateral pterygoid plate damaged
7/244	N	F	-	-	-	-	-	-	-	-	0	0	-	-	Incomplete ossification of of the auditory yubes, incl. ff. of Hushke bilaterally; f in R SO notch
11/242	-	-	-	-	-	-	-	-	-	-	-	-		-	
22/533															
23/558															
32/732															
39/714															
40/885	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Only small fragments present
41/744	N	N	L/I/M	L/I/M	0	0	BN	BN	SA	SA	0	0			Huge infraornital foramina, huge greater palatine foramina
42/779	F	N	-	-	-	-	-	-	-	-	-	-	-	-	Foramen spinosum open completely into petrosquamosal fissure
47/1158	N	F	0/I	-	0	0	LN	LN	L	L	0	0			
48/1047	F	F	-	-	-	-	-	-	-	-	-	-		-	Foramen of Hushke on right side
53/1194															
59/1225	1F 1N	1F 1N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
62/1297	-	N	-	L/I/M	-	0	-	-	-	-	-	-		-	Pterygospinous bridging on left, two infraorbital foramina on right
64/1422	2F	-	-	-	-	-	-	-	-	-	-	-	-	-	Foramen spinosum opens into petrosquamosal fissure; f. of Hushke on left
70/1476															
71/1475	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly preserved; foramen of Hushke on right
72/1483	F	F	-	-	-	-	-	-	-	-	-	-	-	-	Poor preservation
79/1607															
80/1628	F	F	0/I/M	-	0	0	LN	LN	L	L	-	-			

SPECIMEN	AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen		Palate shape
			L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R	
81/1642	A	M	-	-	-	MO	-	L	-	-	-	-	-	-	-	-	L	-	-	-	-	-	-	-	-
83/1653	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
85/1658	A	M	-	-	-	-	-	-	-	-	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
101/1675			N/0	-	MO	-	M	-	-	-	0	-	-	-	0	M	M	-	-	-	-	-	-	-	-
105/1687			-	-	-	-	S	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
108/1696	A	M	-	-	LO	LO	M	M	-	-	-	-	-	-	-	L	L	0	0	0	0	-	OD	OD	-
110/1699	A	M?	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
117/1765	AD	F	-/0	-/0	SR	SR	S	S	-	-	0	-	-	-	-	M	M	+S	+S	+S	-	-	-	OD	-
118/309			-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
119/299	AD	M	-	-	-	-	-	-	-	-	-	0	-	-	-	-	-	+	+	-	-	-	-	-	-
121/1773	A	M	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
126/1793			-	-	LO	LO	M	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	OD	-	-
*/818			N/0	-	-	-	M	-	M	-	-	-	-	-	-	M	M	-	0	-	-	-	OD	-	-
69/1473	A	F	-	-	-	-	-	-	-	-	-	-	-	-	-	M	M	-	-	-	-	-	-	-	-
89/1668	A	F	-	-	MR	-	M	-	-	-	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
109/1697																									
111/1752																									
112/1753																									
113/1758																									
114/1759																									
115/1761																									
116/1764																									
120/1770																									
122/1774																									
125/1781																									

SPECIMEN	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
	L	R	L	R	L	R	L	R	L	R	L	R	R	L	
81/1642	-	N	-	-	-	-	-	-	-	-	-	-	-	-	Poor preservation
83/1653	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Missing
85/1658	F	F	-	-	-	-	LN	LN	-	-	-	-		-	
101/1675	N	N	-	-	-	-	-	-	-	-	0	0	-	-	Left foramen spinosum opens into petrosquamosal fissure; poor preservation
105/1687	-	F	-	-	-	-	-	-	-	-	-	-	-	-	
108/1696	F	N	L/I	L++/I/M	+	+	EN	EN	-	SA	0	0			
110/1699	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Very badly preserved - only small fragments
117/1765	N	-	-	-	-	-	-	-	-	-	-	-	-	-	Both ff. spinosa open into fissures; foramen in SO notch on left
118/309	F	F	L/I/M	L/I/M	0	0	BD	BD	SA	SA	-	-		-	
119/299	N	-	-	-	-	-	-	-	-	-	-	-	-	-	
121/1773	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Very poorly preserved
126/1793	F	F	-	-	-	-	-	-	-	-	0	0	-	-	Very poorly preserved
*/818	N	N	L/I	-	0	0	BN	-	SA	-	-	-	-		Left foramen ovale almost bridged; right f. spinosum opens into fissure
69/1473	F	F	L/I/M	-	+	-	LN	-	SA	-	0	0	-		Foramina of Hushke preset bilaterally; relatively well preserved
89/1668	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
109/1697															
111/1752															
112/1753															
113/1758															
114/1759															
115/1761															
116/1764															
120/1770															
122/1774															
125/1781															

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen		Palate shape
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R	
34/762		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	L	-	-	-	-	-	-	-	-
46/1045																										
60/1257		A	M	-	-	MO	-	M	-	-	-	-	-	0	-	0	L	L	-	-	-	-	-	-	-	-
77/*																										
78/1499																										
128/1789		A	M	-	-	-	-	M	M	-	-	-	-	0	-	-	M	M	-	-	-	-	-	-	-	-
129/1791		A	M	-	-	-	-	-	-	-	-	-	-	0	-	-	-	M	-	-	-	-	-	-	-	-
82/1643		A	F	-	-	-	-	M	-	-	-	-	-	0	-	-	-	-	-	-	-	-	-	-	-	-
138/2318		A	F	-	-	-	-	-	-	-	-	0	0	0	0	0	L	L	-	-	-	-	-	-	-	-
24/564																										

SPECIMEN	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
	L	R	L	R	L	R	L	R	L	R	L	R	R	L	
34/762	N	-	-	-	-	-	-	-	-	-	0	-	-	-	Poor preservation
46/1045															
60/1257	F	N	-	-	-	-	-	-	-	-	-	-	-	-	Bones of the face badly damaged
77/*															
78/1499															
128/1789	N	N	-	-	-	-	-	-	-	-	-	-	-	-	R. f. spinosum opens into pterygosquamosal fissure; ff. of Hushke present bilaterally
129/1791	N	N	-	-	-	-	-	BN	-	-	-	-	-	-	Poor preservartion
82/1643	-	-	-	L+/I/M	-	0	-	EN	-	A	-	-		-	Damaged
138/2318	F	F	L/I	L/I	0	0	AN	AN	A	A	-	-			Right supraorbital formen very laterally placed
24/564															

APPENDIX D

COMPARATIVE DATA COLLECTED FROM THE PERRY SITE SAMPLE

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
93		A	M	-	-	MO	MO	M	M	M	M	0	0	0	0	0	M	M	+	+	+	+	BEHIND	-	RD
99		A	M	-	-	MO	MO	S	S	L	L	0	-	-	-	-	L	L	0	0	0	0	-	-	OD
111		A	M	-	-	-	-	-	-	M	M	0	0	0	0	0	DAM	DAM	+	+	+	+	BEHIND	OD	OS
115		A	M	-	-	LO	LO	M	M	-	-	-	-	-	-	-	M	M	+	+	+	+	-	OS	OS
114		A	M	-	-	MO	MO	S	S	L	L	0	L	L	0	0	DAM	DAM	+	+	+	+	-	RD	OD
112		A	F	-	-	-	MR	-	M	-	-	-	M	M	-	-	M	M	0	0	0	0	-	OD	OD
113		A	F	-	-	MO	MO	M	M	-	-	-	-	-	-	-	L	-	+	+	+	+	-	OD	OD
127		A	M	-	-	-	LR	-	M	-	-	-	-	-	-	-	-	L	+	-	-	-	-	-	-
128		A	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	OS	OS
130		A	F	-	-	MO	MO	M	M	-	-	-	-	-	-	-	L	L	0	0	0	0	-	-	-
131		A	M	-	-	DAM	DAM	DAM	DAM	-	-	-	S	S	-	-	M	M	-	-	-	-	-	-	-
132		A	?	-	-	-	-	-	-	-	-	-	-	-	-	-	DAM	DAM	+	+	+	+	-	OD	OD
133		A	F	-	-	LO	DAM	L	L	-	-	-	-	-	-	-	M	M	0	0	0	0	-	-	-
140		A	F	N/0	-	MO	-	M	-	-	-	-	-	M	-	-	-	M	0	0	0	0	-	OD	OS
137		A	F	-	N/0	LO	-	M	-	-	-	-	-	-	-	-	DAM	DAM	+	-	+	-	-	OD	RD
182A		A	F	-	-	MO	MO	M	M	-	-	-	-	-	-	-	-	S	0	0	0	0	-	OS	OS
182B		A	?	-	-	MO	MO	M	M	-	-	-	-	-	-	-	M	M	0	0	0	0	EVEN	OS	OS
183		A	F	-	N/0	-	MO	M	M	M	M	0	M	M	0	0	L	L	+	+	+	+	-	OD	OD
215		A	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
216		A	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
220		A	M	-	-	-	LO	-	M	-	-	-	M	M	-	-	M	M	+	0	0	0	-	DAM	OS
252		A	F	-	-	MO	-	M	-	-	-	-	-	-	-	-	M	M	+	+	0	0	-	DAM	OD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
93	MODSLPOINT	N	N	0/I/M	0/I/M	+	+	-	-	A	A	0	0	-		
99	-	N	N	0/I/M	0/I/M	0	0	-	-	SA	SA	0	0	-	-	Damaged
111	MODPOINT	N	N	0/I/M	L/I/M	DAM	DAM	UD	UD	DAM	DAM	-	-			
115	-	N	N	L/I/M	L/I/M	+	+	-	-	A	A	0	0	-	-	Partially reconstructed
114	-	N	BOTH	0/I/M	0/I/M	0	0	UN	-	SA	SA	0	0		-	Damaged
112	-	N	N	L/I/M	L/I/M	+	+	-	-	A	A	0	0	-	-	
113	-	DAM	DAM	0/I/M	0/I/M	0	DAM	LN	-	SA	SA	-	-			
127	-	N	N	L/I/M	L/I/M	+	+	UD	UD	SA	SA	0	0			
128	-	BOTH	N	DAM	0/I/M	+	+	UN	UN	DAM	DAM	0	0			Partially reconstructed
130	-	BOTH	N	L/I/M	-	+	-	UD	UD	SA	-	-	-			
131	-	N	N	-	-	-	-	-	-	-	-	-	-	-	-	Damaged
132	-	F	F	L/I/M	L/I/M	+	+	UN	-	-	-	-	-			In pieces
133	-	BOTH	BOTH	-	-	-	-	-	-	-	-	-	-	-	-	Foramen spinosum at end of spine; damaged
140	-	BOTH	BOTH	0/I/M	0/I/M	0	0	-	-	-	-	-	-	-	-	Damaged
137	-	F	F	-	0/I/M	-	0	-	UD	-	-	-	-	-		Damaged
182A	-	-	-	L/I/M	L/I/M	+	+	-	-	SA	SA	0	0	-	-	
182B	-	-	-	0/I/M	0/I/M	-	0	-	-	SA	SA	0	0	-	-	
183	MODBLUNT	-	-	0/I/M	0/I/M	-	0	-	-	SA	SA	0	0	-	-	
215	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Too damaged
216	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Too damaged
220	-	F	F	L/I	L/I	+	+	UN	-	A	A	-	-		-	Very wide nasal aperature
252	-	N	N	0/I/M	0/I/M	0	0	-	-	SA	SA	0	0		-	

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
253		A	M	-	-	MR	MO	M	M	-	-	-	-	-	-	-	L	L	+	+	+	+	-	-	-
254		A	F	-	-	LO	LO	M	M	-	-	-	-	-	-	-	M	M	0	+S	+	+	-	-	OD
288		A	F	N/0	N/0	MO	MO	S	S	-	-	-	-	-	0	-	-	-	-	-	-	-	-	-	-
296		A	M	-	-	MO	MO	L	L	M	M	0	DAM	DAM	0	+	DAM	DAM	0	0	+	+	BEHIND	OD	OD
289		A	F	-	-	-	-	-	-	-	-	-	-	-	-	-	S	DAM	0	0	0	0	-	OS	OS
297		J	?	W/0	W/0	MO	MR	M	L	L	L	0	0	0	0	0	L	L	0	0	0	0	BEHIND	SD	SD
307		A	F	N/0	N/0	MO	MO	M	M	M	M	0	0	0	0	0	L	L	+	+	0	0	BEHIND	OS	OS
304		A	M	-	-	LO	LO	L	L	L	L	0	L	L	0	0	M	M	+	+	+	+	VBEHIND	RD	OD
305		?	?	-	-	MO	MO	M	M	-	-	-	-	-	-	-	-	-	+	DAM	+	DAM	BEHIND	DAM	RD
310		A	M	-	-	LO	LO	L	L	DAM	DAM	0	M	M	0	0	M	M	+	+	0	0	-	OD	OD
309		A	F	N/0	N/0	MO	MO	M	M	-	-	-	-	-	-	-	-	-	0	0	0	0	-	OD	OD
312		A	F	W/0	-	MO	-	S	-	-	-	-	-	-	-	-	M	M	+	+	+	+	-	OD	OS
311		A	M	N/0	N/0	MO	MO	M	M	M	M	0	-	L	0	0	-	L	0	0	0	0	BEHIND	OS	OS
314		A	M	N/0	N/0	MO	MO	M	M	-	-	-	M	DAM	-	-	M	DAM	+	+	+	+	-	OD	OD
313		J	M	-	-	-	-	-	-	-	-	-	-	DAM	-	-	S	DAM	-	-	-	-	-	-	-
315		A	M	-	-	-	LO	M	M	-	-	-	-	DAM	-	-	DAM	DAM	+	+	+	+	-	RD	OD
317		A	F	W/0	W/0	LO	LO	M	M	-	-	-	-	-	-	-	L	M	+	DAM	+	DAM	-	OD	-
316		A	F	N/0	N/0	MO	MO	M	M	-	-	-	-	-	-	-	-	-	0	0	0	0	-	OS	OS
319		A	M	-	-	-	MO	-	L	M	M	0	M	M	0	0	L	L	+	+	+	+	BEHIND	OD	OD
318		A	F	N/0	N/0	LO	LO	M	M	-	-	-	-	-	-	-	DAM	DAM	0	0	0	0	-	OD	OD
320		A	M	-	-	-	MO	-	L	M	M	-	0	0	-	-	-	-	DAM	DAM	DAM	DAM	BEHIND	-	-
321		A	F	-	-	MO	MO	M	M	-	-	-	-	-	-	-	-	-	+	+	+	+	-	OS	OS

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
253	-	-	-	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-	-	
254	-	-	-	-	L/I/M	-	+	-	UN	-	-	-	-	-		Damaged
288	-	-	-	L/I/M	L/I/M	+	+	-	-	SA	SA	0	0		-	
296	THICKPOINT	N	N	-	-	-	+	LD	LD	-	SA	0	+		-	Reconstructed
289	-	N	BOTH	L/I/M	L/I/M	+	+	-	-	A	A	-	-	-	-	
297	MODPOINT	-	-	0/I/M	0/I/M	0	0	-	-	SA	SA	0	0	-	-	
307	-	N	BOTH	L/I/M	L/I/M	+	+	-	-	SA	A	-	-	-	-	
304	THICKPOINT	N	N	L/I/M	L/I/M	+	+	UD	UD	SA	SA	0	0			Damaged
305	-	-	-	L/I/M	L/I/M	+	+	-	-	A	A	0	0	-	-	Damaged
310	MODBLUNT	N	N	0/I/M	L/I/M	0	0	-	-	SA	SA	-	-	-	-	Both ff. ovales open into fissure
309	-	N	N	0/I/M	0/I/M	0	0	-	-	SA	SA	0	0	-	-	
312	-	N	N	L/I/M	L/I/M	+	+	UN	UN	SA	SA	-	-			
311	-	-	-	0/I/M	0/I/M	0	0	-	-	A	A	-	-	-	-	
314	-	-	N	0/I/M	0/I/M	0	0	-	-	SA	SA	0	0	-	-	
313	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Badly damaged
315	-	F	F	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-	-	
317	-	-	-	L/I/M	L/I/M	+	+	-	-	SA	SA	-	-	-	-	
316	-	-	-	L/I/M	L/I/M	0	0	-	-	L	L	0	0		-	
319	MODPOINT	N	F	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-	-	
318	-	-	-	L/I/M	L/I/M	+	+	-	-	SA	SA	-	-	-	-	
320	MODPOINT	F	N	L/I	L/I	+	+	UN	UN	A	A	-	-			Good preservation
321	-	-	-	L/I/M	-	+	-	-	-	SA	-	-	-	-	-	

SPECIMEN		AGE	SEX	Lateral pterygoid plate		Ovale		Spinosum		Foramen lacerum		Spur @ basion	Jugular process		Jugular foramen bifurcated		Postglenoid plate		Palatal spurs		Palate ridge		Vomer relative to sphenooccipital synchondrosis	Greater palatine foramen	
				L	R	L	R	L	R	L	R		L	R	L	R	L	R	L	R	L	R		L	R
322		A	F	-	-	MO	MO	M	M	-	-	-	-	-	-	-	M	M	+	0	+	0	-	OD	OD
347		A	M	N/0	N/0	MO	LO	M	M	-	-	-	-	-	-	-	M	L	-	-	-	-	-	-	-
351		A	M	N/0	N/0	MO	MO	M	M	-	-	-	-	-	-	-	DAM	L	DAM	-	-	-	-	-	-
359		A	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-
360		A	F	-	N/0	-	MO	-	DAM	DAM	DAM	0	-	-	-	-	DAM	DAM	0	0	+	+	EVEN	DAM	RD
358		A	F	-	-	MO	-	-	M	-	-	-	-	-	-	-	M	-	0	0	0	0	-	OD	OD
361		A	F	-	-	-	DAM	-	-	-	-	-	-	-	-	-	M	-	-	-	-	-	-	-	-
362		A	F	-	-	DAM	DAM	DAM	DAM	-	-	-	-	-	-	-	DAM	L	-	-	-	-	-	-	-
436		A	M	DAM	-	DAM	DAM	DAM	DAM	-	-	-	-	-	-	-	M	M	+	+	+	+	-	OD	SD
443		A	F	-	DAM	DAM	LO	-	S	-	-	-	-	-	-	-	-	-	+	+	+	+	-	OD	OD
74		A	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	-	OD	OD
94		A	M	DAM	DAM	-	-	-	-	-	-	-	-	-	-	-	L	L	+	+	+	+	-	OD	OD
86		A	M	-	-	DAM	DAM	DAM	DAM	-	-	-	-	-	-	-	-	-	0	0	0	0	-	OD	OD
87		A	M	-	-	LO	LO	S	L	DAM	M	0	0	0	0	0	L	L	+	+	+	+	VBEHIND	RS	RS
84		A	M	DAM	DAM	MO	MO	M	M	M	M	0	-	-	-	-	L	-	DAM	+	DAM	+	-	OS	-
97		A	M	W/+	W/-	-	DAM	-	DAM	-	-	-	-	-	-	-	L	DAM	-	+	-	+	-	-	OD
76		A	M	-	-	-	DAM	-	DAM	-	-	-	-	-	-	-	M	M	+	-	+	-	-	OD	-
72		A	M	W/+	W/+	-	MO	-	M	-	-	-	-	-	-	-	L	M	+	+	+	+	-	OD	OD

SPECIMEN	Palate shape	Supraorbital foramen/notch		Infraorbital foramen		Infraorbital margin		Zygomatic tubercle		Infraorbital margin angle		Trochlear spur		Zygomatic suture		Notes
		L	R	L	R	L	R	L	R	L	R	L	R	R	L	
322	-	-	-	0/I/M	-	0	-	-	-	-	-	-	-	-	-	
347	-	N	N	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-	-	Damaged
351	-	N	F	-	L/I/M	-	+	-	-	-	SA	0	0	-	-	
359	-	-	-	0/M	0/M	0	0	-	-	SA	SA	-	-	-	-	
360	THICKBLUNT	N	N	-	-	-	-	UN	UN	SA	SA	-	-	-	-	Reconstructed
358	-	F	N	L/I/M	L/I/M	+	+	-	-	SA	SA	-	-	-	-	
361	-	DAM	DAM	L/I/M	-	+	-	-	-	SA	-	-	-	-	-	Very fragmented
362	-	N	N	0/I/M	DAM	+	+	DAM	LD	A	A	0	0		-	Metopic suture patent
436	-	F	N	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-		Occipital bone flat
443	-	N	N	L/I/M	L/I/M	+	+	UD	UD	SA	SA	0	0			Foramen of Huschke on left
74	-	-	N	0/I/M	0/I/M	0	0	-	-	SA	SA	-	-	-	-	Fragmented
94	-	2F	BOTH	L/I/M	L/I/M	+	+	-	UN	SA	SA	0	0	-		
86	-	BOTH	BOTH	0/I/M	0/I/M	0	0	-	-	A	A	0	0	-	-	
87	DAM	N	N	-	-	-	+	-	DAM	-	SA	0	0	-	-	Left f. spinosum at end of spine
84	-	N	2F1N	-	L/I/M	-	+	UD	-	SA	SA	-	-		-	
97	-	N	BOTH	L/I/M	L/I/M	+	+	UN	-	SA	SA	0	0		-	
76	-	BOTH	BOTH	0/I/M	0/I/M	0	0	UN	-	SA	SA	-	-		-	
72	-	2F	2F	L/I/M	L/I/M	+	+	UN	-	SA	SA	-	-		-	

APPENDIX E

COMPARISON OF CHARACTER PRESENCE IN ALL FOUR SAMPLES

Character	Spitlafields						Terry					
	Left		Right		Mid		Left		Right		Mid	
	Ratio	%	Ratio	%	Ratio	%	Ratio	%	Ratio	%	Ratio	%
Lateral pterygoid bridging	14/277	0.05	9/277	0.03			2/60	0.03	3/60	0.05		
Indeterminate (?)	-	-	1/277	0.00			-	-	-	-		
Missing/Damaged	108/277	0.39	116/277	0.42			-	-	-	-		
Ovale												
SR	1/277	0.00					1/60	0.02	0/59	0.00		
SO	10/277	0.04	7/277	0.03			2/60	0.03	1/59	0.02		
MR	12/277	0.04	13/277	0.05			8/60	0.13	6/59	0.10		
MO	109/277	0.39	109/277	0.39			18/60	0.30	21/59	0.36		
LR	16/277	0.06	24/277	0.09			8/60	0.13	8/59	0.14		
LO	39/277	0.14	40/277	0.14			23/60	0.38	23/59	0.39		
Indeterminate (?)	-	-					-	-	-	-		
Missing/Damaged	88/277	0.32	102/277	0.37			-	-	1/59	0.02		
Spinosum												
S	40/178	0.22	41/171	0.24			12/58	0.21	17/59	0.29		
M	110/178	0.62	98/171	0.57			40/58	0.69	35/59	0.59		
L	28/178	0.16	32/171	0.19			6/58	0.10	7/59	0.12		
Indeterminate (?)	-	-	1/277	0.00			1/58	0.02	-	-		
Missing/Damaged	99/277	0.36	105/277	0.38			1/58	0.02	1/60	0.02		
Foramen Lacerum												
S	49/170	0.29	55/167	0.33			29/60	0.48	29/58	0.50		
M	98/170	0.58	89/167	0.53			24/60	0.40	22/58	0.38		
L	23/170	0.14	23/167	0.14			7/60	0.12	7/58	0.12		
Indeterminate (?)	1/277	0.00	1/277	0.00			-	-	-	-		
Missing/Damaged	106/277	0.06	109/277	0.39			-	-	2/60	0.03		
Spur at Basion					2/201	0.01					0/60	0
Indeterminate (?)					1/277	0.0036					-	-
Missing/Damaged					75/277	0.2708					-	-
Jugular Process												
0	150/174	0.86					23/60	0.38	23/60	0.38		
S	1/174	0.01					10/60	0.17	10/60	0.17		
M	19/174	0.11					24/60	0.40	25/60	0.42		
L	4/174	0.02					3/60	0.05	2/60	0.03		
Indeterminate (?)	2/277	0.01					-	-	-	-		
Missing/Damaged	101/277	0.36					-	-	-	-		
Jugular foramen bridged	16/176	0.09	22/175	0.13			9/60	0.15	6/60	0.10		
Indeterminate (?)	1/277	0.00	1/277	0.00			-	-	-	-		
Missing/Damaged	100/277	0.36	101/277	0.36			-	-	-	-		
Posteglenoid plate												
S	30/192	0.16	23/187	0.12			5/55	0.09	2/55	0.04		
M	91/192	0.47	86/187	0.46			25/55	0.45	27/55	0.49		
L	71/192	0.37	78/187	0.42			25/55	0.45	26/55	0.47		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	85/277	0.31	90/277	0.32			5/60	0.08	5/60	0.08		
Palatal Spurs	98/178	0.55	98/176	0.56			42/60	0.70	44/60	0.73		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	99/277	0.36	97/277	0.35			1/60	0.02	-	-		
Palatal Ridge	59/157	0.38	59/155	0.39			52/60	0.87	45/60	0.75		
Indeterminate (?)							-	-	-	-		
Missing/Damaged	120/277	0.43	115/277	0.42			-	-	-	-		
Vomer												
Behind					75/174	0.431					15/60	0.25
Even					94/174	0.5402					31/60	0.5167
Beyond					4/174	0.02					14/60	0.2333

Character	Spitlafields						Terry					
	Left		Right		Mid		Left		Right		Mid	
Indeterminate (?)					2/277	0.01					-	-
Missing/Damaged					102/277	0.36					-	-
Gr. Palatine foramen												
OD	42/169	0.25	39/170	0.23			20/60	0.33	20/59	0.34		
OS	47/169	0.28	50/170	0.29			9/60	0.15	8/59	0.14		
RD	15/169	0.09	15/170	0.09			8/60	0.13	6/59	0.10		
RS	27/169	0.16	23/170	0.14			4/60	0.07	6/59	0.10		
SD	15/169	0.09	16/170	0.09			12/60	0.20	12/59	0.20		
SS	23/169	0.14	26/170	0.15			7/60	0.12	6/59	0.10		
Indeterminate (?)	-	-					-	-	1/60	0.02		
Missing/Damaged	108/277	0.39	107/277	0.39			-	-	-	-		
Supraorbital foramen/notch												
Foramen	33/193	0.17	38/192	0.20			13/60	0.22	11/60	0.18		
Notch	139/193	0.72	123/192	0.6406			39/60	0.65	37/60	0.62		
Both	20/193	0.10	30/192	0.16			8/60	0.13	12/60	0.20		
Indeterminate (?)	1/277	0.00	1/277	0.00			-	-	-	-		
Missing/Damaged	84/277	0.30	85/277	0.30			-	-	-	-		
Infraorbital foramen												
0/I/M	3/151	0.02	2/155	0.01			2/60	0.03	2/60	0.03		
0/I	1/151	0.01	2/155	0.01			0/60	0.00	0/60	0.00		
L/I	48/151	0.32	28/155	0.18			13/60	0.22	8/60	0.13		
L/M	7/151	0.05	14/155	0.09			9/60	0.15	9/60	0.15		
L/I/M	92/151	0.61	109/155	0.70			36/60	0.60	41/60	0.68		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	126/277	0.56	122/277	0.44			-	-	-	-		
Infraorbital margin	92/154	0.60	99/153	0.65			34/60	0.57	48/60	0.80		
Indeterminate (?)	-	-	1/277	0.00			-	-	-	-		
Missing/Damaged	123/277	0.44	124/277	0.45			-	-	-	-		
Zygomatic Trubercle												
BD	17/142	0.12	19/138	0.14			3/60	0.05	3/60	0.05		
BN	1/142	0.01	1/138	0.01			21/60	0.35	22/60	0.37		
LD	51/142	0.36	50/138	0.36			2/60	0.03	2/60	0.03		
LN	30/142	0.21	27/138	0.20			19/60	0.32	18/60	0.30		
UD	23/142	0.16	23/138	0.17			4/60	0.07	4/60	0.02		
UN	20/142	0.14	18/138	0.13			11/60	0.18	11/60	0.18		
Indeterminate (?)	1/277	0.01	1/277	0.00			-	-	-	-		
Missing/Damaged	134/277	0.48	138/277	0.50			-	-	-	-		
Infraorbital magrin angle												
A	37/155	0.24	34/148	0.23			25/60	0.42	26/60	0.43		
SA	85/155	0.55	83/148	0.56			31/60	0.52	30/60	0.48		
L	32/155	0.21	30/148	0.20			3/60	0.05	3/60	0.05		
Indeterminate (?)	1/277	0.00	1/277	0.01			1/60	0.02	1/60	0.02		
Missing/Damaged	121/277	0.44	128/277	0.46			-	-	-	-		
trochlear spur	7/174	0.04	14/174	0.08			4/60	0.07	2/60	0.03		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	103/277	0.37	102/277	0.37			-	-	-	-		

Character	Campbell's Farm						Perry Site					
	Left		Right		Mid		Left		Right		Mid	
	Ratio	%	Ratio	%	Ratio	%	Ratio	%	Ratio	%	Ratio	%
Lateral pterygoid bridging	2/7	0.29	0/5	0.00			2/21	0.10	1/22	0.05		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	32/39	0.82	34/39	0.87			47/62	0.76	46/62	0.74		
Ovale												
SR	1/16	0.06	0/14	0.00			0/34	0.00	0/38	0.00		
SO	1/16	0.06	2/14	0.14			0/34	0.00	0/38	0.00		
MR	5/16	0.31	4/14	0.29			1/34	0.03	2/38	0.06		
MO	3/16	0.19	3/14	0.21			25/34	0.74	24/38	0.71		
LR	1/16	0.06	1/16	0.06			0/34	0/34	1/38	0.03		
LO	5/16	0.31	4/14	0.29			8/34	0.24	11/38	0.29		
Indeterminate (?)	-	-	-	-			-	-				
Missing/Damaged	23/39	0.59	25/39	0.59			28/62	0.45	24/60	0.40		
Spinosum												
S	2/17	0.12	1/12	0.08			5/33	0.15	4/39	0.10		
M	11/17	0.65	8/12	0.67			24/33	0.73	29/39	0.74		
L	4/17	0.24	3/12	0.25			4/33	0.12	6/39	0.15		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	22/39	0.56	27/39	0.69			29/62	0.47	23/62	0.37		
Foramen Lacerum												
S	1/4	0.25	1/3	0.33			0/13	0.00	0/14	0.00		
M	3/4	0.75	2/3	0.67			9/13	0.69	10/14	0.71		
L	0/4	0.00	0/3	0.00			4/13	0.31	4/14	0.29		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	35/39	0.90	36/39	0.92			49/62	0.79	48/62	0.77		
Spur at Basion					0/9	0.00					0/15	0.00
Indeterminate (?)					-	-					-	-
Missing/Damaged					30/39	0.77					47/62	0.76
Jugular Process												
0	3/39	0.08	4/39	0.10			7/15	0.47	7/16	0.44		
S	0/39	0.00	0/39	0.00			1/15	0.07	1/16	0.06		
M	0/39	0.00	0/39	0.00			5/15	0.33	6/16	0.38		
L	0/39	0.00	0/39	0.00			2/15	0.13	2/16	0.13		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	36/39	0.92	35/39	0.90			47/62	0.76	46/62	0.74		
Jugular foramen bridged	0/4	0.00	1/39	0.03			0/12	0.00	1/12	0.08		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	35/39	0.90	32/39	0.82			50/62	0.81	50/62	0.81		
Posteglenoid plate												
S	0/27	0.00	0/28	0.00			2/33	0.06	1/33	0.03		
M	16/27	0.59	15/28	0.54			18/33	0.55	18/33	0.55		
L	11/27	0.41	13/28	0.46			13/33	0.39	14/33	0.42		
Indeterminate (?)	-	-	-	-			-	-	-			
Missing/Damaged	12/39	0.31	11/39	0.28			29/62	0.47	29/62	0.47		
Palatal Spurs	3/6	0.50	4/8	0.50			29/49	0.59	26/46	0.57		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	30/39	0.77	31/39	0.79			13/62	0.21	16/62	0.26		
Palatal Ridge	3/6	0.50	3/6	0.50			29/49	0.59	25/46	0.54		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	31/39	0.79	31/39	0.79			13/62	0.21	16/62	0.26		
Vomer												
Behind					2/2	1.00					11/13	0.85
Even					0/2	0.00					2/13	0.15
Beyond					0/2	0.00					0/13	0.00

Character	Campbell's Farm						Perry Site					
	Left		Right		Mid		Left		Right		Mid	
Indeterminate (?)					-	-					-	-
Missing/Damaged					37/39	0.95					49/62	0.79
Gr. Palatine foramen												
OD	5/7	0.71	6/6	1.00			25/37	0.65	24/44	0.55		
OS	1/7	0.14	0/6	0.00			9/37	0.24	13/44	0.30		
RD	0/7	0.00	0/6	0.00			3/37	0.08	4/44	0.09		
RS	0/7	0.00	0/6	0.00			1/37	0.03	1/44	0.02		
SD	1/7	0.14	0/6	0.00			1/37	0.03	2/44	0.05		
SS	0/7	0.00	0/6	0.00			0/37	0.00	0/44	0.00		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	32/39	0.82	33/39	0.85			23/62	0.37	18/62	0.29		
Supraorbital foramen/notch												
Foramen	15/27	0.56	14/26	0.54			9/40	0.23	7/42	0.17		
Notch	11/27	0.41	11/26	0.42			25/40	0.63	25/42	0.60		
Both	1/27	0.04	1/26	0.04			6/40	0.15	10/42	0.24		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	12/39	0.31	13/39	0.33			22/62	0.35	20/62	0.32		
Infraorbital foramen												
0/I/M	1/9	0.11	0/7	0.00			23/49	0.47	23/49	0.47		
0/I	1/9	0.11	0//7	0.00			2/49	0.09	0/49	0.00		
L/I	3/9	0.33	1/7	0.14			2/49	0.04	2/49	0.04		
L/M	0/9	0.00	0//7	0.00			0/49	0.00	0/49	0.00		
L/I/M	4/9	0.44	6/7	0.86			22/49	0.45	24/49	0.49		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	30/39	0.77	32/39	0.82			13/62	0.21	13/62	0.21		
Infraorbital margin	2/11	0.18	1/11	0.09			26/47	0.55	28/50	0.56		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	28/39	0.72	28/39	0.72			15/62	0.24	12/62	0.19		
Zygomatic Trubercle												
BD	1/10	0.10	1/10	0.10			0/18	0.00	0/14	0.00		
BN	2/10	0.20	2/10	0.20			0/18	0.00	0/14	0.00		
LD	0/10	0.00	0/10	0.00			1/18	0.06	2/14	0.14		
LN	6/10	0.60	6/10	0.60			1/18	0.06	0/14	0.00		
UD	0/10	0.00	0/10	0.00			6/18	0.33	6/14	0.43		
UN	1/10	0.10	1/10	0.10			10/18	0.56	6/14	0.43		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	29/39	0.74	29/39	0.74			44/62	0.71	48/62	0.77		
Infraorbital magrin angle												
A	1/9	0.11	2/7	0.29			10/47	0.21	11/47	0.23		
SA	6/9	0.67	3/7	0.43			36/47	0.77	35/47	0.74		
L	2/9	0.22	2/7	0.29			1/47	0.02	1/47	0.02		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	30/39	0.77	32/39	0.82			15/62	0.24	15/62	0.24		
trochlear spur	0/8	0.00	0/7	0.00			0/26	0.00	1/26	0.04		
Indeterminate (?)	-	-	-	-			-	-	-	-		
Missing/Damaged	31/39	0.79	32/39	0.82			36/62	0.58	36/62	0.58		

APPENDIX F

INITIAL OBSERVATIONS OF THE SPITALFIELDS SAMPLE

2022 – Badly damaged specimen. Bony spurs present on palate. Infraorbital foramina round in shape.

2063 – Edentulous. Infraorbital foramen round, lipped laterally. Large postglenoid plates. This cranium does not have the same hyperostotic traits that others seem to have.

2070 – Infraorbital foramina oval with lip. Trochlear spur in right orbit. "Stepped" zygomaticomaxillary sutures. Huge postglenoid plates. Large pterygoid hamuli. Small spurs/ridges on hard palate. Both foramen lacerum small. Large postcondylar fossae/foramina. Lateral pterygoid plate has bridging growth.

2098 – Arched zygomaticomaxillary sutures. Oval infraorbital foramina with great amount of lipping. Small spurs and ridges on palate. Long, skinny pterygoid hamuli. Huge right mastoid foramen. Large postcondylar fossa. Occipital looks like it has a supraeniac ridge. Bridging growth on lateral pterygoid plate.

2099 – Infraorbital groove long, deep. One supraorbital foramen and one supraorbital notch on each side. Very deep tear-drop shaped lacrimals. Mastoid foramen very large; two one left side. "Stepped" zygomaticomaxilary sutures. Palatal spurs, sharp ridges on palate bone. Small sphenoid hamuli. Small foramina lacera. Left condylar foramen absent. Position of foramen ovale and foramen spinosum similar to others in sample. The right lateral pterygoid plate "bridged" in a tight loop – similar to 2098.

2124 – No fissures in petrosals. Normal carotid canal. Medial pterygoid plate beyond the basiocciput and lateral. Hypermasculine characters, with what looks like an occipital keel/supereniac depression. Squared-off zygoma. Possible accessory condylar foramen just lateral to left occipital condyle. Temporal line is high on the cranium. Infraorbital canal open into maxillary sinus.

2134 – Zygomatic suture “stepped” in appearance. Bony spurs on lateral palate, just anterior to the palatine foramina. Medial pterygoid plate just beyond the spheno-occitpital synchondrosis and flared laterally.

Figure G.1: Spitalfields specimen 2134

2139 – Adolescent, age 16. Bony spurs on palate. Zygomaticomaxillary suture almost straight angle. Medial pterygoid plates even with basiocciput and not flared laterally. Cribra orbitalia present. Infraorbital foramina almost covered by the eversion or “rolled appearance” of the infraorbital margin. Hamuli of the pterygoid are large and stocky. Condylar foramina and condylar fossae large.

Figure G.2: Spitalfields specimen 2139

2142 – Infraorbital foramina look similar to the ones on 2139 – aimed downward and almost covered by the rolled infraorbital margins. Zygomaticomaxillary suture arched in appearance, and patent from the floor of the orbit down to the infraorbital foramen. Great deal of hyperostotic activity on both jugular processes. Large bony ridges on the hard palate. Bone at asterion present.

Figure G.3: Spitalfields specimen **2142**

2152 – Older individual, completely edentulous. Infraorbital foramen shape is again oval, pointed down, and somewhat covered by the rolled infraorbital margin. Shape of the zygomaticomaxillary suture is slightly stepped. Medial pterygoid plates lateral and beyond the basiocciput. Pterygoid hamuli short and stubby. Great deal of alveolar resporption.

2162 – Overall shape of the cranium is round, with flared zygomas. Infraorbital foramina round. Zygomaticomaxillary suture obliterated. Multiple bony spurs on palate. Large ridge/spine by (on right) and between (on left) of the lesser palatine foramina. Growth on jugular processes. Huge foramina in the nasal bones. Large postglenoid plate. Huge condylar fossae. Medial pterygoid plates lateral and beyond spheno-occipital synchondrosis. Very large hamuli. Very robust individual overall.

2163 – Spurs on palate, sharp ridges on palate bones. Oval-shaped infraorbital foramina. Slightly arched zygomaticomaxillary sutures. Growth on jugular processes. Medial pterygoid plate lateral and beyond s-o synchondrosis. Long skinny hamuli. Medial orbital walls perforated with many foramina. Probably an older individual; sagittal suture obliterated; but retained most of the teeth. Vomer alae a strange shape, square almost, and not fused. Very wide digastric notch.

2166 – Growth on jugular processes. Infraorbital foramina round; 2 on each side. Bony spurs on palate, low ridge. Arched zygomaticomaxillary sutures. Hamuli damaged.

2167 – Infraorbital foramina round-shaped. Distinct brow ridge, especially at glabella. Single pointed turbercles on inferior margins of zygomatic bones. Asymmetrical appearance of the face, with the right eye seemingly placed lower than the left. Nasal bones peaked, high. Rather different growth lateral to the occipital condyles; left anterior condylar foramen bridged. Long, skinny hamuli. Bony growth on the posteriolateral portion of the lateral pterygoid plates. Palate has deep grooves and distinct bony spurs. Bony spurs on mastoid processes. Medial plate beyond and lateral relative to the spheno-occipital synchondrosis. Lesser and greater palatine foramina separated by small but sharp ridges. Large anterior condylar foramina.

2169 – Infraorbital foramina oval with axis on horizontal. Palatal spurs; low, sharp palatal ridge. Zygomaticomaxillary sutures stepped. Bony spurs on palate, low sharp ridges. Bony growth around both foramina rotunda; left one has a “loop” of bone over it. Rough growth on jugular processes. Hamuli long and curved. Huge right mastoid foramen. Both sides have supraorbital notches and foramen. Palatine torus present, more prominent on right side of the hard palate. Sagittal and coronal sutures almost obliterated.

Figure G.4: Spitalfields specimen 2169

2171 – Metopic stuture patent. Bony growths above infraorbital foramen. Trochlear spurs present. Bony spurs and sharp ridges present on palate bones. No growth on jugular processes. Zygomaticomaxillary suture has two components, horizontal and vertical – os japonicum. Medial pterygoid plate beyond the spheno-occipital synchondrosis. Individual is completely edentulous.

2173 – Left zygomaticomaxillary suture curved, right stepped in appearance. Infraorbital foramina narrow and oval shaped on inferiosuperior axis; bony lip lateral on both. Pterygospinous bridging on right, over foramen ovale and spinosum. Extensive growth on jugular processes – facet present on right where the growth and atlas were in contact. Large foramina lacera. Spur of growth at the anterior border of the foramen magnum. Medial pterygoid plates beyond the spheno-occiptial synchondrosis.

Figure G.5: Spitalfields specimen 2173

2175 – Very small individual, but adult. Zygomaticomaxillary sutures straight, but angled. Cribra orbitalia present in both orbits. Bony spurs on palate; sharp bony ridges on palate bones separating greater and lesser palatine foramina. Uncompleted pterygospinous/basal bridging on right side. No prominent growths on jugular processes. Huge postcondylar plates. Small hamuli on medial pterygoids. Medial pterygoid plates beyond the spheno-occipital synchondrosis and not flared laterally in their appearance.

2178 – Zygomaticomaxillary sutures slightly curved. Infraorbital foramina round; three on each side of the face. No spurs or ridges on palate. Huge jugular foramina. Tiny hamuli on medial pterygoids. Bony growth on the anterior portion of the sphenoid. Slight bumpy growth next to the occipital condyles. Medial pterygoid plates beyond the spheno-occiptital synchondrosis and lateral (flared).

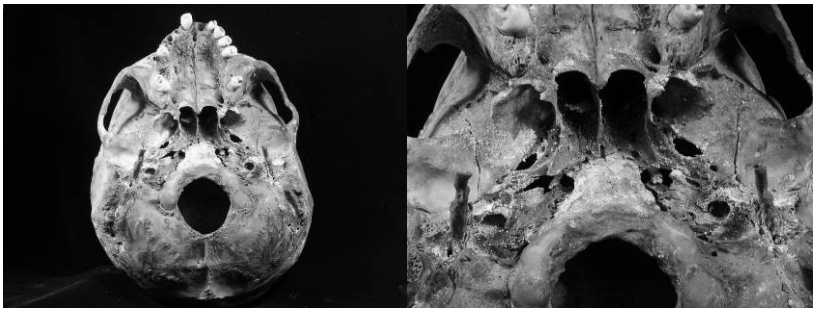


Figure G.6: Spitalfields specimen 2978

2181 – Not at all well-preserved. Overall a broad skull. Broad, flat zygomas/appearance to the face. Large, round infraorbital foramina. Large mastoid foramina. Small postglenoid plates.

Figure G.7: Spitalfields specimen 2181

2182 – Broad face. Large lateral pterygoid plates. No postglenoid plates present. Both supraorbital notches and foramina present on both sides. Lozenge-shaped lacrimal grooves. Bony spurs and slight ridges on palate. Right foramen spinosum seems to be absent. Foramina of Huschke present bilaterally. Superiomedial portion of orbital rim angled inferiomedially. Thick zygomatic bones. Infraorbital foramina “half-moon” in shape. Inferior nasal border smooth

and sloped. Both foramina ovale bridged over with bone, but different than other observations of pterygospinous bridging in the sample – not as robust. Left foramen spinosum almost positioned in glenoid fossa. Greater palatine foramina very large, deep, and funnel-shaped. Thyroid cartilage ossified.

Figure G.8: Spitalfields specimen 2182

2184 – Head appears to be very broad; basicranium narrow. Large postglenoid plates. Right foramen spinosum bridged with bone. Lacrimal grooves teardrop-shaped. Zygomatic bones swept back and up. Zygomaticomaxillary sutures stepped, and then curve downward. Huge apical abscesses on the right posterior portion of the alveolus; moved into the maxillary bone. Short, thick pterygoid hamuli. Long alveolus/maxilla. Infraorbital foramina open inferiorly – thick bone inferior to the orbit. Basicranium wide – wide distance between foramen magnum and the mastoid processes.

Figure G.9: Spitalfields specimen 2184

2186 – Deep canine fossae, “exaggerated” zygomas. Edentulous. Infraorbital foramina open inferiorly, and are very close to the inferior border of the orbits. Posterior

nasal spine thick and rounded. Right foramen spinosum bridged. Hamuli of the medial pterygoids broken. Right petrosal damaged. Large postcondylar plates. Deep, round greater palatine foramen. Large, stout left styloid process.

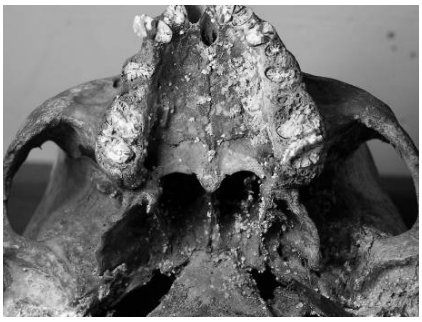


Figure G.10: Spitalfields specimen 2186

2187 – Inferior borders of the zygomatic bones level with two tubercle-like protrusions. Zygomaticomaxillary sutures acutely angled. Deep canine fossae. Large infraorbital foramina; seem distant from inferior margins of orbits. Sharp ridges on palate bones, no bony spurs present on palate. Thin palate bones, thick and pointed posterior nasal spine. Long, thick hamuli. Lateral pterygoid plates appear to be normal. Small postcondylar plates. Large and round greater palatine foramen. Long and narrow hard palate. Medial pterygoid plates even with the spheno-occipital synchodrosis, and not flared laterally. Alae of vomer even with the medial pterygoid plates. Foramina ovales and rotundae look normal. Thick ridge along the occiput mediolaterally, resembling an occipital keel.

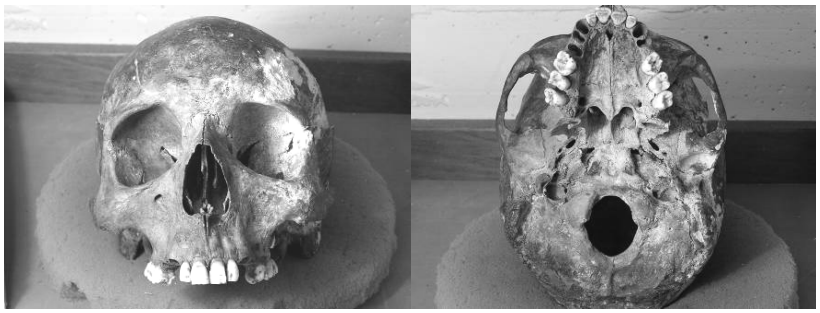


Figure G.11: Spitalfields specimen 2187

2189 – Left zygomatic bone slightly thinker than the right. Slight spurs and ridges on the palate. Left lateral pterygoid plate normal, right growth wide extending past the foramen spinosum. Long, skinny hamuli on the medial pterygoid plates. Large foramina lacera. Very large lacrimal grooves. Medial pterygoid plates even with the spheno-occipital synchondrosis and not laterally flared. Alae of the vomer do not reach the spheno-occipital synchondrosis.

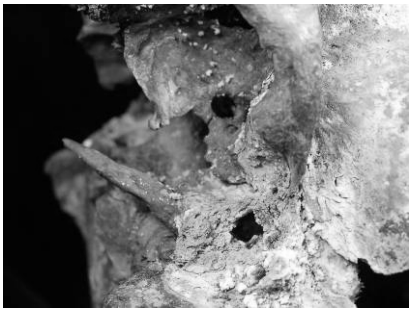


Figure G.12: Spitalfields specimen 2189

2192 – Skull similar in overall appearance to specimen 2184, having narrow basicranium and wide clavarium. Infraorbital foramina very narrow, almost slits; positioned at angle. Inferior border of zygomatic bones level; two small tubercles. Bony spurs on hard palate. Greater palatine foramina slit-like in appearance. Pterygoid plates appear normal. Medial pterygoid plates lateral beyond the spheno-occipital synchondrosis. Foramina ovales look normal. Foramina spinosa right next to petrosals. Very small foramina lacera. Narrow palatine torus along midline of the hard palate. Short, skinny hamuli. Medium postcondylar plates. Large right mastoid foramen.

2203 – Robust male. Circular infraorbital foramina. Zygomaticomaxillary suture stepped superiorly, angled laterally inferiorly. Lacrimal grooves teardrop-shaped. Very deep palate. Bony spurs and sharp ridges on hard palate. Deep, oval-shaped greater palatine foramina. Large mastoid foramina. Large postglenoid plates. Right foramen spinosum almost bifurcated. Left foramen spinosum opens against petrosal. Foramina ovales normal. Left mastoid notch very wide.

Face wide in overall appearance. Thyroid cartilage ossified. A single, large incisive foramen; appearance may be due to the presence of periodontal disease.

Figure G.13: Spitalfields specimen 2203

2204 – Round infraorbital foramina. Inferior borders of the zygomas swept up and back. Orbits very square in appearance – others in sample seem to be more rhomboidal. Broad, shallow palate. Smaller, shallow greater palatine foramina. Small spurs on hard palate. Short, thin hamuli. Very narrow lateral pterygoid plates. Normal foramina ovales and rotunda. Slight palatine torus. Lacrimal fossa lozenge-shaped. Alae of vomer do not reach back to spheno-occipital synchondrosis. Medial pterygoid plates reach beyond the spheno-occipital synchondrosis, and are flared laterally.

Figure G.14: Spitalfields specimen 2204

2205 – Skull is in excellent condition. Trochlear spur in right orbit. Both sides have both supraorbital notches and foramina. Zygomaticomaxillary sutures are arched/curved. Inferior margins of the zygomatic bones swept up and back.

Spurs and ridges on hard palate. Deep, slit-like greater palatine foramina. Small postglenoid plates. Short, thick hamuli. Left foramen ovale and spinosum open next to the petrous portion of the temporal. Right foramen ovale normal, right foramen spinosum missing. Large mastoid foramina. Medial pterygoid just beyond and lateral. Overall palate seems short anterioposteriorly. Alae of the vomer do not reach back to the spheno-occipital synchondrosis. Ossified thyroid cartilage.

2207 – Asymmetrical appearance of face. Large, narrow infraorbital foramina. Inferior border of right zygoma level, with two small tubercles. Zygomaticomaxillary sutures stepped. Large, deep lacrimal fossae. Palate long anterioposteriorly. Very small foramina lacera. Foramen ovales and rotunda normal appearance. Bony spurs and sharp ridges on palate bones. Very deep palatine foramina.

2211 – Great deal of taphonomic damage. Slight bony spurs and ridges on palate bones. Deep palate/tall alveolus Very deep, funnel-shaped greater palatine foramina. Hamuli damaged, but seem to have been small. Medial pterygoid plates are just beyond and lateral. Thin lateral pterygoid plates. Patent metopic suture.

2216 – Completely reduced to dust. Demonstrates the wide variation in preservation found in the Spitalfields sample.

2221 – Another specimen in a horrible state of preservation, but the thyroid cartilage is ossified.

2223 – Another badly preserved specimen. Large foramina lacera. Both foramina rotunda open into the respective petrosal.

2231 – Edentulous, alveolus almost completely resorbed. Inferior border of the zygomas level. Slit-like Infraorbital foramina. Lozenge-shaped lacrimal fossae.

Deep, triangular, tear-drop greater palatine foramina. Wide pterygoid plates. Left foramen spinosum bridged. Alae of vomer do not reach the spheno-occipital synchondrosis. Medial pterygoid plates just beyond and somewhat flared laterally. Small postglenoid plates. Thick, robust styloid processes. Long, thick hamuli. Large and multiple mastoid processes.

Figure G.15: Spitalfields specimen 2231

2243 – Badly preserved. "Normal-looking" foramina ovales and spinosa. Large postglenoid plates. Alae of the vomer do reach the spheno-occiptial synchondrosis. Medial pterygoid plates just beyond and lateral. Trochlear spur in right orbit.

2244 – Narrow face, back of skull wide. Inferior border of the zygomatic bones swept up and back. Lateral pterygoid plates appear normal. Medial pterygoid plates beyond and lateral. Alae of vomer reaches spheno-occipital synchondrosis. Slight spurs on palate, no ridges. Medium-sized postglenoid plates. Slit-like and shallow greater palatine foramina. Huge mastoid foramina.

2246 – Edentulous. Orbits square-shaped in appearance. Deep and long infraorbital grooves. Large, horizontally-oriented infraorbital foramina. Two infraorbital foramina on right. Inferior border of the zygomatic bones slight angle up. Deep palate. Right greater palatine foramen teardrop in shape, left oval, both deep. Short, thick hamuli. Foramina ovales and right spinosum normal, no foramen spinosum on left. Alae of vomer do not reach the spheno-oocipital

synchondrosis. Medial pterygoid plates beyond and somewhat flared laterally. Ossified thyroid cartilage.

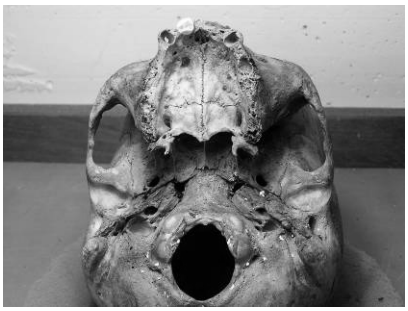


Figure G.16: Spitalfields specimen 2246

2251 – Low, level inferior borders of the zygomas, with two small tubercles on each side. Trochlear spur in the right orbit. Round infraorbital foramina. Huge post glenoid plates. Spur of bone intruding into the foramen magnum from the anterior border of the foramen. Deep diagastric notches. Foramina ovales round. Unusual shape to palate bones. Edentulous.

Figure G.17: Spitalfields specimen 2251

2255 – Inferior borders of the zygomatic bones slope upward. Infraorbital foramina semicircular, open inferiorly. Lacrimal fossae large and lozenge-shaped. Deep palate/tall alveolus. Round, shallow greater palatine foramina. Small spurs on hard palate, no ridges present. Relatively wide lateral pterygoid plates. Alae of vomer reaches spheno-occiptial synchondrosis. Medial pterygoid plates just beyond and lateral. Short, stubby hamuli. Huge right mastoid foramen, exsutral,

on occipital; left mastoid foramen is insutural. Deep digastric notches. Huge left jugular foramen.

2259 – Infraorbital foramina crecent-shaped; right points medially, left points inferiorly. Angled zygomatic sutures. Wide palate. Lateral pterygoid pates very wide. Left foramen ovale bridged – bridging from most superior portion of the lateral pterygoid plate. Bridging extends over the left foramen spinosum as well. Hamuli are short and hooked. Slight spurs and sharp ridges on the palate. Huge styloid processes. Alae of the vomer do not quite reach the spheno-occipital synchondrosis. Medial pterygoid plates even with the spheno-occipital synchondrosis and flared laterally. Little spurs on the superior margin of the external auditory meatuses.

2272 – Edentulous. Inferior border of the zygomatic bones level with two small tubercles. Infraorbital foramina oval, horizontally oriented, open inferiorly. Palate appears to have been deep, but not sure because of the amount of alveolar resorption. Deep, oval greater palatine foramina. Wide lateral pterygoid plates. Small hamuli. Foramina ovales and spinosa appear normal. Medial pterygoid plates beyond and lateral. Two bony spurs anterior to the occipital condyles. Alae of the vomer touching the spheno-occiptial synchondrosis. Huge left mastoid foramen. Lacrimal areas damaged. Huge left jugular foramen.

Figure G.18: Spitalfields specimen 2272

2281 – Badly damaged. Each side has both supraorbital foramina and notches. Lateral pterygoid plates damaged. Alae of the vomer do not reach the spheno-occipital

synchondrosis. Greater palatine foramina shallow and slit-like in appearance. Medial pterygoid plates beyond and lateral. Thick styloid processes. Huge mastoid foramen.

2291 – Infraorbital foramina open inferiorly. Wide zygomatic bones. Right infraorbital groove long. Lacrimal fossae tear-dropped shaped. Palate is deep and long. Shallow, oval greater palatine foramina. Alae of the vomer reach the spheno-occipital synchondrosis. Small hamuli. Left lateral pterygoid plate damaged, right lateral pterygoid plate very wide. Medial pterygoid plates beyond and lateral. Relatively large postglenoid plates. Small bony spurs on palate.

2295 – Infraorbital foramina open inferiomedially. Inferior borders of the zygomatic bones level. Shallow, oval greater palatine foramina. Inferior portion of the lateral pterygoid plates very broad. Large pterygopalatine foramina. Bony spurs projecting into the "pterygoid fissure." Small foramina lacera. Alae of the vomer reach the spheno-occipital synchondrosis.

Figure G.19: Spitalfields specimen 2295

2296 – Metopic suture patent. Infraorbital foramina open inferiorly. Orbits are square in shape. Inferior border of the right zygoma slightly angled upward, left level. Small, shallow, oval greater palatine foramina. Wide lateral pterygoid plates. Alae of vomer do not reach the spheno-occipital synchondrosis. Medial pterygoid plates just beyond and lateral. Foraman of Huscke present on right petrosal.

2298 – Eversion of or “rolled appearance” to the infraorbital margins. Multiple supraorbital foramina on both sides, with wide supraorbital notches. Lacrimal fossae large and lozenge-shaped. Trochlear spur in right orbit. Infraorbital foramina open inferiomedially. Zygomatic bones slope up and back. Large palatine torus. Deep palate. Oval, shallow greater palatine foramina. Short, fat hamuli. Right lateral pterygoid plate is very wide. Mastoid foramina exsutural and on occiput. Huge vaginal processes around styloid processes. Large right pterygopalatine foramen.

2300 – Both sides have supraorbital foramina and notches. Thick, rolled infraorbital borders. Inferior border of zygomas level, with two small tubercles. Zygomaticomaxillay sutures angled. Infraorbital foramina open medially. Edentulous; shallow palate. Medial pterygoid plates just beyond and lateral. Mastoid foramina insutural. Greater palatine foramina shallow and slit-like.

Figure G.20: Spitalfields specimen 2300

2301 – Huge postglenoid plates. Left foramen ovale opens into the “petrosal fissure.” Small foramen present above each external auditory meatus. Moderately deep palate. Shallow greater palatine foramina. Level zygomas. Infraorbital foramina open inferiomedially. Zygomaticomaxillary sutures angled.

2496 – In poor condition. Huge mastoid foramen on right. Huge postglenoid plates. Huge styloid processes as well.

2498 – Infraorbital foramina “half-moon” shaped, oriented vertically and open medially. Convex inferior border of the zygomatic bone. Pterygospinous bridging on left, both the foramen ovale and spinosum bridged. The right foramen spinosum almost bridged, but incomplete. Wide lateral pterygoid plates. Small stubby hamuli. Small bony spurs on palate. Greater palatine foramina deep, oval, funnel-shaped. Zygomaticomaxillary sutures stepped and angled.

Figure G.21: Spitalfields specimen 2498

2500 – Very well preserved. Very wide lateral pterygoid plates. Long, hooked hamuli. Huge postglenoid plates, extend over part of petrosals. Sharp, distinct ridges on palate; no spurs. Huge mastoid foramina. Two infraorbital foramina on both sides; round in shape. Narrow zygomas with concave inferior borders. Medial pterygoid plates beyond and greatly flared laterally. Very tiny styloid processes. Slit-like, shallow greater palatine foramina.

Figure G.22: Spitalfields specimen 2500

2501 – Very damaged, especially the right side. Infraorbital foramina half-moon shaped and opens medially, oriented vertically. Zygomaticomaxillary sutures angled.

Medial pterygoid plates beyond and lateral. Relatively wode lateral pterygoid plates. Right side has both a supraorbital foramen and supraorbital notch. Right foramen spinosum small, right next to ovale.

2507 – Bones of the face and basicranium damaged. Pterygoid plates wide, damaged. Large right mastoid foramen. Medial pterygoid plates just beyond and lateral. Small spurs on palate, no ridges. Greater palatine foramina deep, round, and funnel-shaped.

Figure G.23: Spitalfields specimen 2507

2510 – Badly damaged, left side somewhat intact. No spurs, ridges on palate. Narrow lateral pterygoid plates. Small greater palatine foramina. Hamuli long and skinny.

2515 – Overall robust individual; broad skull. Small lateral pterygoid plates. Broad, flat basicranium. Medial pterygoid plates even and not flared laterally. Large postglenoid plates. Big mastoid foramina. Large, but stumpy mastoids.

Figure G.24: Spitalfields specimen 2515

2518 – Both sides have a supraorbital foramen and supraorbital notch. Infraorbital foramina positioned very close to the inferior border of the orbits. Inferior borders of the zygomas level, small tubercles. Small spurs on palate, sharp ridges. Greater palatine foramina deep, oval, funnel-shaped. Large postglenoid plates. Deep diagastric notches. Small foramina lacera. Right hamulus short and curled, left damaged. Medial pterygoid plate just beyond and not flared laterally. Zygomas are not flared. Incomplete pterygospinous bridging.

2519 – Skull slightly deformed, probably the result of forces after burial (taphonomic). Sharp spurs on palate, sharp ridges around lesser palatine foramina. Long, thin hamuli. Grooves from the incisive foramina to the middle of the palate bones. Foramen ovales and spinosa located lateral to the lateral pterygoid plates. Partial pterygospinous bridging on right. Large vaginal processes. Small postglenoid plates. Zygomaticomaxillary suture angles inferiolaterally. Lacimal fossae teardrop-shaped. Small tubercles on inferior margin of the zygomatic bones. Infraorbital foramina position is close to the inferior border of the orbits. Deep canine fossae; “rolled” infraorbital borders.

Figure G.25: Spitalfields specimen 2519

2524 – Both sides have a supraorbital foramen and notch. Infraorbital foramina half-moon shaped, open inferiomedially. Right foramen ovale very large and round. Wide lateral pterygoid plates. Small ridges and spurs on palate. Relatively small foramina lacera. Hamuli broken. Medial pterygoid plates beyond the spheno-

occipital synchondrosis and not flared laterally. Deep and wide digastric notches. Very large post glenoid plates.

2526 – Left side has both the supraorbital foramen and notch, right just the notch. Right zygomatic taller inferiosuperiorly than the left, creating an asymmetrical appearance to the face. Infraorbital foramina half-moon shaped. Greater palatine foramina slit-like, deep. Spurs and sharp ridges on palate. Right foramen ovale round and large. Right foramen spinosum bridged with loop of bone. Wide lateral pterygoid plates. Large postglenoid plates. Hamuli long and thin.

Figure G.26: Spitalfields specimen 2526

2527 – Inferior margin of the zygomatic bones roughened, tubercle-like protrusions. Lacrimal grooves appear to be particularly shallow. Small bony spurs on hard palate. Greater palatine foramen deep and funnel-shaped. Broad, triangular hamuli. Pterygospinous bridging over right ovale. Wide lateral pterygoid plates. Position of the right foramen spinosum is significantly lateral, almost in glenoid fossa. Large foramina lacera. Bone at asterion on right. Large post glenoid plates. Right jugular foramen bifurcated. Both jugular foramina very large. Left digastric notch very deep. Deep postcondylar fossa. Multiple mastoid foramina on both sides. Narrow and vertically oriented infraorbital foramina. Zygomaticomaxillary sutures from an obtuse angle. Both sides have both a supraorbital notch and foramen.

Figure G.27: Spitalfields specimen 2527

2528 – Facial bones, left petrosal damaged, but present. Right jugular foramen is very large, with large intrusion into petrosal displacing the carotid foramen anteriorly. Pterygoid damaged, but appear to be narrow. Foramina ovales and spinosa very close together.

2534 – Pterygospinous bridging over right foramen ovale. Wide lateral pterygoid plates. Large jugular foramina. Growth on jugular processes. Large foramina lacera. Medial pterygoid plate beyond the spheno-occipital synchondrosis and lateral. Left side of the skull is missing. Distinct ridge along the horizontal plane of the occipital bone, resembling an occipital torus. Large postglenoid plates.

Figure G.28: Spitalfields specimen 2534

2535 – Inferior border of zygomatic bones smooth. "Normal-looking" foramina ovales and spinosa. Thin lateral pterygoid plates. Large jugular foramina. Distinct occipital condyles, with an inferiorly convex shape. Long, narrow hamuli. Narrow, triangular palate. Bony spurs and ridges on palate bones. Large

mastoid foramina. Deep mastoid notches. Large trochlear spur in right orbit. Right side of the mandible is missing. Edentulous.

Figure G.29: Spitalfields specimen 2535

2538 – Deep, distinct lacrimal grooves. Zygomaticomaxillary sutures almost obliterated; stepped in appearance. Left side has both supraorbital foramen and notch. Two tubercle-like structures on the inferior margin of the zygomatic bones. Lateral right pterygoid plate damaged; both narrow in appearance. No bony spurs or ridges on palate. Large postglenoid plate. "Normal-looking" foramina ovales and spinosa. Large mastoid foramina. Temporozygomatic suture wide/open, probably due to damage. Only right hamulus present, small. Right portion of palate in tact, left missing. Huge right greater palatine foramen. Distinct gonial regions in the mandible; very flared.

Figure G.30: Spitalfields specimen 2538

APPENDIX G

KNOWN FAMILIAL RELATIONSHIPS OF THE INDIVIDUALS FROM THE SPITALFIELDS SKELETAL SAMPLE

Modified from data given by Dr. Louise Humphrey of the Natural History Museum, London, and from the Spitalfields publications sponsored for online publication at Archaeological Data Services by the Friends of Christchurch Spitalfields. http://ads.ahds.ac.uk/catalogue/resources.html?spitalfields_var_2001.

ID	Specimen	Used	Surname	Relationship
8	2008	√	BOWDEN	FATHER OF 477 & 542.
477	2477	√	BOWDEN	DAUGHTER OF 008. SISTER OF 542.
542	2542	√	BOWDEN	BROTHER OF 477. SON OF 008.
24	2024	√	FOWLER	FATHER OF 624.
624	2624		FOWLER	SON OF 024.
63	2063	√	PONTARDENT	FATHER OF 203, GRANDFATHER OF 206. PROBABLY GREAT GRANDFATHER OF 065, PROBABLY HALF SISTER OF 184, SAME FATHER. 'HALF UNCLE' OF 249,250,175 & 188.
203	2203	√	PONTARDENT	SON OF 063, FATHER OF 206, HUSBAND OF 070, PROBABLY GRANDFATHER OF 065, 'HALF NEPHEW' OF 184, 'HALF COUSINS' OF 249, 250, 175 & 188.
206	2206		PONTARDENT	SON OF 070 & 203, GRANDSON OF 063, PROBABLY UNCLE OF 065, DISTANT RELATION OF 184, 249, 250, 175 & 188.
70	2070	√	PONTARDENT	WIFE OF 203, MOTHER OF 206, PROBABLY GRANDMOTHER OF 065.
65	2065		PONTARDENT	PROBABLY GRANDAUGHTER OF 070 & 203. PROBABLY NEICE OF 206. PROBABLY GREAT GRANDAUGHTER OF 063, PROBABLY RELATION OF 184,249,250,175 & 188.
162	2162	√	LEMAISTRE	HUSBAND OF 184, FATHER OF 249, 250, 175 & 188, BROTHER OF 211 & 207, SON OF 204.
175	2175	√	LEMAISTRE	DAUGHTER OF 162 & 184, SISTER OF 249, 250 & 188, GRANDAUGHTER OF 204, NEICE OF 211 & 207, 'HALF NEICE' OF 063, 'HALF COUSIN' OF 203, DISTANT RELATIVE OF 206 & 065.
184	2184	√	LEMAISTRE	WIFE OF 162, MOTHER OF 249, 250, 175 & 188, HALF SISTER OF 063, 'HALF AUNT' OF 203, & DISTANT RELATIVE OF 065 & 206.
188	2188		LEMAISTRE	DAUGHTER OF 162 & 184, SISTER OF 249, 250, & 175, GRANDAUGHTER OF 204, NEICE OF 211 & 207, 'HALF NEICE' OF 063,'HALF COUSIN' OF 203, DISTANT RELATIVE OF 206 & 065.
249	2249		LEMAISTRE	DAUGHTER OF 162 & 184, SISTER OF 188, 250 & 175, GRANDAUGHTER OF 204, NEICE OF 211 & 207, 'HALF NEICE' OF 063, 'HALF COUSIN' OF 203, DISTANT RELATIVE OF 206 & 065.
250	2250		LEMAISTRE	DAUGHTER OF 162 & 184, SISTER OF 249, 188 & 175, NEICE OF 211 & 207, 'HALF NEICE' 063, OF GRANDAUGHTER OF 204,'HALF COUSIN' OF 203, RELATIVE OF 206 & 065.

ID	Specimen	Used	Surname	Relationship
104	2104	√	WHITE	BROTHER OF 112.
112	2112	√	WHITE	SISTER OF 104.
129	2129	√	CHEVALIER	GRANDFATHER OF 133. HUSBAND OF 137.
137	2137		CHEVALIER	GRANDMOTHER OF 133. WIFE OF 129.
133	2133	√	CHAUVET	SON OF LEWIS CHAUVET, GRANDSON OF 137 & 129.
330	2330		DAYCOCK	FATHER OF 461 & 142. POSSIBLY GRANDFATHER OF 545.
142	2142	√	DAYCOCK	SISTER OF 461, DAUGHTER OF 330. POSSIBLY AUNT OF 545.
461	2461	√	DAYCOCK	BROTHER OF 142, SON OF 330. POSSIBLY FATHER OF 545.
545	2545	√	DAYCOCK	POSSIBLY SON OF 461.
171	2171	√	LEMERE	POSSIBLY FATHER OF 187.
187	2187	√	LEMERE	POSSIBLY SON OF 171.
850	2850	√	HARWOOD	HUSBAND OF 192, FATHER OF 613.
192	2192	√	HARWOOD	WIFE OF 850, MOTHER OF 613.
613	2613	√	HARWOOD	SON OF 850 AND 192.
948	2948	√	KILNER	HUSBAND OF 949, FATHER OF 205 & 916.
949	2949		KILNER	WIFE OF 948, MOTHER OF 205 & 916.
205	2205	√	KILNER	SISTER OF 916.DAUGHTER OF 949 & 948?
916	2916		KILNER	POSSIBLY SON OF 948 & 949, & BROTHER OF 205.
955	2955		MESMAN	HUSBAND OF 263, FATHER OF 244 & 954, FATHER IN LAW OF 259 & 243, GRANDFATHER OF 254 & 255 & 304, GREAT GRANDFATHER OF 698 & 327, GREAT GREAT GRANDFATHER OF 242.
263	2263	√	MESMAN	WIFE OF 955, MOTHER OF 244 & 954, MOTHER IN LAW OF 259 & 243, GRANDMOTHER OF 254 & 255 & 304, GREAT GRANDMOTHER OF 698 & 327, GREAT GREAT GRANDMOTHER OF 242.
244	2244	√	MESMAN	SON OF 955 & 263, BROTHER OF 954, HUSBAND OF 259, FATHER OF 254, 255 & 304, FATHER IN LAW OF 956, GRANDFATHER OF 698 & 327,GREAT GRANDFATHER OF 242, BROTHER IN LAW OF 243.

ID	Specimen	Used	Surname	Relationship
259	2259	√	MESMAN	WIFE OF 244, MOTHER OF 255, 254 & 304, GRANDMOTHER OF 698 & 327, DAUGHTER IN LAW OF 955 & 263, SISTER IN LAW OF 954 & 243, MOTHER IN LAW OF 956, GREAT GRANDMOTHER OF 242.
254	2254		MESMAN	SON OF 244 & 259, BROTHER OF 304 & 255, BROTHER IN LAW OF 956, UNCLE OF 698, GRANDSON OF 955 & 263, NEPHEW OF 954, UNCLE OF 327, GREAT UNCLE OF 242.
255	2255	√	MESMAN	SON OF 244 & 259, BROTHER OF 254 & 304, FATHER OF 698, HUSBAND OF 956, GRANDSON OF 955 & 263, NEPHEW OF 954, UNCLE OF 327, GREAT UNCLE OF 242.
698	2698	√	MESMAN	DAUGHTER OF 255, GREAT GRANDAUGHTER OF 955 & 263, GRANDAUGHTER OF 244 & 259, GREATNEICE OF 954, NEICE OF 304 & 254, COUSIN OF 327, 1ST COUSIN ONCE REMOVED OF 242.
304	2304		MESMAN	SON OF 244 & 259, BROTHER OF 254 & 255, BROTHER IN LAW OF 956, UNCLE OF 698, NEPHEW OF 954, GRANDSON OF 955 & 263, GRANDFATHER OF 242, FATHER OF 327.
954	2954		MESMAN	HUSBAND OF 243, SON OF 955 & 263, BROTHER OF 244, BROTHER IN LAW OF 259, UNCLE OF 304, 255 & 254, GREAT UNCLE OF 698 & 327, GREAT GREAT UNCLE OF 242.
243	2243	√	COX	WIFE OF 954, SISTER IN LAW OF 244 & 259, DAUGHTER IN LAW OF 955 & 263, AUNT IN LAW OF 304, 255 & 254.
327	2327	√	JOURDAN	MOTHER OF 242, DAUGHTER OF 304, NEICE OF 255 & 254, GRANDAUGHTER OF 244 & 259, GRANDNEICE OF 954, GREAT GRANDAUGHTER OF 955 & 263, COUSIN OF 698.
242	2242		JOURDAN	SON OF 327, GRANDSON OF 304, GREAT NEPHEW OF 255 & 254, GREAT GRANDSON OF 244 & 259, GREAT GREAT NEPHEW OF 954, GREAT GREAT GRANDSON OF 955 & 263, 1ST COUSIN ONCE REMOVED OF 698.
464	2464	√	WILLIAMS	POSSIBLY FATHER OF 381, GRANDFATHER OF 503 & 264.
381	2381	√	WILLIAMS	POSSIBLY SON OF 464.
264	2264		WILLIAMS	BROTHER OF 503, GRANDSON OF 464.
503	2503		WILLIAMS	SISTER OF 264, GRANDAUGHTER OF 464.
340	2340	√	MEGNIN	FATHER OF 277, 374 & 441.
277	2277		MEGNIN	SON OF 340, BROTHER OF 441 & 374.
374	2374		MEGNIN	SISTER OF 441 & 277, DAUGHTER OF 340.
441	2441		MEGNIN	BROTHER OF 374 & 277. SON OF 340.
439	2439	√	DICKENS	FATHER OF 580 AND GRANDFATHER OF 278.
580	2580	√	DICKENS	FATHER OF 278, AND SON OF 439.
278	2278		DICKENS	SON OF 580 AND GRANDSON OF 439.

ID	Specimen	Used	Surname	Relationship
283	2283		WILLIAMS	POSSIBLY SISTER OF 512.
512	2512		WILLIAMS	POSSIBLY BROTHER OF 283.
296	2296	√	GARDINER	POSSIBLY MOTHER OF 572.
572	2572		GARDINER	POSSIBLY SON OF 296.
502	2502	√	LAY	HUSBAND OF 437. FATHER OF 302.
437	2437	√	LAY	WIFE OF 502, MOTHER OF 302.
302	2302		LAY	SON OF 437 & 502.
547	2547		LAY	TWIN BROTHER TO 549.
549	2549		LAY	TWIN BROTHER TO 547.
309	2309		COURTAULD	SISTER OF 863, 789, AND 609, AUNT OF 527 & 720, GREATAUNT OF 467.
609	2609	√	JULIEN	SISTER OF 789, 309, 863, AUNT OF 527 & 720, GREAT AUNT OF 467, STEP-MOTHER OF 956.
789	2789	√	MERZEAU	SISTER OF 863, 609 & 309, MOTHER OF 527, GRANDMOTHER OF 467, AUNT OF 720.
527	2527	√	MERZEAU	SON OF 789, FATHER OF 467, COUSIN OF 720, NEPHEW OF 863, 309 & 609.
467	2467		THISELTON	DAUGHTER OF 527, GRANDAUGHTER OF 789, GREAT NEICE OF 609, 309 & 863, 1ST COUSIN ONCE REMOVED OF 720, COUSIN OF 728, 474, 797, 796, 771, 463 & 833.
863	2863	√	OGIER	BROTHER OF 789 & 609 & 309. UNCLE OF 527 & 720, GREAT UNCLE OF 467.
671	2671	√	SOREL	FATHER OF 797, 796, 463 & 771.
463	2463		SOREL	SON OF 671, BROTHER OF 771, 796 & 797. COUSIN OF 833, 728, 474 & 467.
771	2771		SOREL	DAUGHTER OF 671, SISTER OF 796, 463 & 797. COUSIN OF 833, 728, 474 & 467.
796	2796		SOREL	SON OF 671, BROTHER OF 797, 463 & 771. COUSIN OF 833, 728, 474 & 467.
797	2797		SOREL	DAUGHTER OF 671, SISTER OF 796, 463 & 771. COUSIN OF 833, 728, 474 & 467.
714	2714	√	GAMAGE	FATHER OF 728 & 474.
474	2474	√	GAMAGE	SON OF 714, AND BROTHER OF 728, COUSIN OF 797, 796, 771, 463, 833 & 467.
728	2728	√	GAMAGE	SON OF 714, AND BROTHER OF 474. COUSIN OF 797, 796, 771, 463, 833 & 467.
833	2833		LAMBERT	COUSIN OF 797, 796, 771, 463, 728, 474 & 467.

ID	Specimen	Used	Surname	Relationship
493	2493	√	MERCER	GRANDMOTHER OF 334.
334	2334		MERCER	GRANDSON OF 493.
364	2364		BACKER	SISTER OF 440.
440	2440		BACKER	BROTHER OF 364.
371	2371	√	SANDERS	GRANDMOTHER OF 455 & 365.
365	2365		SANDERS	BROTHER OF 455, GRANDSON OF 371.
455	2455		SANDERS	SISTER OF 365, GRANDAUGHTER OF 371
576	2576	√	SAINSBURY	FATHER OF 389 & 368.
368	2368	√	TRIMMER	DAUGHTER OF 576, SISTER OF 389.
389	2389	√	SAINSBURY	SON OF 576, BROTHER OF 368.
369	2369	√	WILLIAMS	POSSIBLY MOTHER OF 373, & 497.
373	2373		WILLIAMS	POSSIBLY BROTHER OF 497, SON OF 369.
497	2497		WILLIAMS	POSSIBLY SISTER OF 373 & DAUGHTER OF 369.
544	2544	√	SMITH	POSSIBLY MOTHER OF 376.
376	2376		SMITH	POSSIBLY SON OF 544.
412	2412		LEESE	SON OF 471.
471	2471		LEESE	MOTHER OF 412.
670	2670	√	JACKSON	MOTHER OF 419.
419	2419	√	JACKSON	SON OF 670.
431	2431		JONES	POSSIBLY BROTHER OF 452.
452	2452		JONES	POSSIBLY BROTHER OF 431.
465	2465	√	SHERMAN	MOTHER OF 453.
453	2453		SHERMAN	SON OF 465.

ID	Specimen	Used	Surname	Relationship
456	2456		STEPHENS	SISTER OF 548 & 505.
505	2505		STEPHENS	BROTHER OF 548 & 456.
548	2548		STEPHENS	SISTER OF 456 & 505.
537	2537	√	CURTIS	FATHER OF 468.
468	2468	√	CURTIS	SON OF 537.
475	2475		HARVERSON	BROTHER OF 560.
560	2560		HARVERSON	SISTER OF 475.
478	2478		CURTIS	POSSIBLY SISTER OF 482.
482	2482		CURTIS	POSSIBLY BROTHER OF 478.
568	2568	√	CURTIS	MOTHER OF 577.
577	2577	√	CURTIS	SON OF 568.
513	2513		BENNETT	SISTER OF 529.
529	2529		BENNETT	SISTER OF 513.
514	2514		STEPHENS	PROBABLY SISTER OF 520.
520	2520		STEPHENS	PROBABLY SISTER OF 514.
579	2579	√	BECK	WIFE OF 749, MOTHER OF 518, GRANDMOTHER OF 628.
749	2749	√	BECK	HUSBAND OF 579, FATHER OF 518, GRANDFATHER OF 628.
518	2518	√	TILSTON	DAUGHTER OF 749 & 579, MOTHER OF 628.
628	2628		TILSTONE	DAUGHTER OF 518, GRANDAUGHTER OF 749 & 579.
621	2621		TAGG	BROTHER OF 737.
737	2737		TAGG	SISTER OF 621.
677	2677	√	RIVAS	POSSIBLY SISTER OF 836.
836	2836		RIVAS	POSSIBLE BROTHER OF 677.
747	2747	√	GALHIE	SISTER OF 903, AUNT OF 768.

ID	Specimen	Used	Surname	Relationship
903	2903	√	ALLEN	BROTHER OF 747, UNCLE OF 768.
768	2768		GALHIE	NEPHEW OF 747 & 903.
792	2792		SMITH	BROTHER OF 815, 877 & 845.
815	2815		SMITH	SISTER OF 845, 877 & 792.
877	2877		SMITH	BROTHER OF 815 & 845 & 792.
926	2926	√	LADBROKE	BROTHER IN LAW OF 939, GREAT UNCLE OF 936.
936	2936	√	LADBROKE	GREAT NEPHEW OF 926.
710	2710	√	LESCHALLAS	WIFE OF 917? 2 JOHN LESCALLAS' LIVED AT THE SAME ADDRESS, OF SIMILAR AGES ONE MARRIED 710, THE OTHER SARAH, ANOTHER J.L. MARRIED MARY.
910	2910	√	LESCHALLAS	SON OF 913 OR 917 ? THERE WERE 3 JOHN LESCHALLAS' AT RED LION COURT OF SIMILAR AGES , WITH THE SAME TRADE, ONE MARRIED SARAH, ANOTHER 710, THE OTHER MARY WHO WAS HIS 2ND WIFE.
913	2913	√	LESCHALLAS	POSSIBLY FATHER OF 910?, THERE ARE SEVERAL JOHN LESCHALLAS'S AROUND AT THE SAME TIME, IMPOSSIBLE TO SORT WITH CERTAINTY. SUSPECT THAT 913, 910 & 917 ARE ALL RELATED BUT UNCLEAR HOW.
917	2917	√	LESCHALLAS	POSSIBLY FATHER OF 910. POSSIBLY HUSBAND OF 710.

BIBLIOGRAPHY

Armelagos GJ, Carlson DS, and Van Gerven DP (1982) The Theoretical Foundations and Development of Skeletal Biology. In F Spencer (ed.): A History of American Physical Anthropology. New York: Academic Press, pp. 305-328.

Ashlock PD (1974) The Uses of Cladistics. Annual Review of Ecology and Systematics *5:*81-99.

Barbujani G, and Sokal RR (1990) Zones of Sharp Genetic Change in Europe Are Also Linguistic Boundaries. Proceedings of the National Academy of Sciences *87:*1816-1819.

Bass WM (1987) Human Osteology: A Laboratory and Field Manual, 3rd Ed. Columbia, Mo.: Missouri Archaeological Society.

Berry AC, and Berry RJ (1967) Epigenetic Variants in the Human Cranium. Journal of Anatomy *101:*361-379.

Berry AC, Berry RJ, and Ucko PJ (1967) Genetical Changes in Ancient Egypt. Man *2:*551-568.

Berry RJ (1963) Epigenetic Polymorphism in Wild Populations of *Mus muslculus*. Genetic Research *4:*193-220.

Berry RJ (1968) The Biology of Non-Metrical Variation in Mice and Men. In DR Brothwell (ed.): The Skeletal Biology of Earlier Human Populations. Oxford: Pergamon Press, pp. 103-133.

Berry RJ, and Searle AG (1963) Epigenetic Polymorphism of the Rodent Skeleton. Proceedings of the Zoological Society of London *140:*577-615.

Blumenbach JF (1795) On the Natural Varieties of Mankind. London: Longman, Green, Roberts, and Green.

Bock WJ (1974) Philosophical Foundations of Classical Evolutionary Classification. Systematic Zoology *22:*375-392.

Boddington A, Garland AN, and Janaway RC, eds. (1987) Death, Decay, and Reconstruction: Approaches to Archaeology and Forensic Science. Manchester: Manchester University Press.

Bowler PJ (1989) Evolution: The History of an Idea. Berkeley: University of California Press.

Brace CL (1982) The Roots of the Race Concept in American Physical Anthropology. In F Spencer (ed.): A History of American Physical Anthropology, 1930-1980. New York: Academic Press, pp. 11-29.

Braga J, Crubezy E, and Elyaqtine M (1998) The Posterior Border of the Sphenoid Greater Wing and Its Phylogenetic Usefulness in Human Evolution. American Journal of Physical Anthropology *107:*387-399.

Broca P (1875) Instructions Craniologiques Et Craniometriqués. Mémoires de la Société d'Anthropologie de Paris, Series 2 *2:*1-204.

Brower AVZ (2002) Cladisitcs, Phylogeny, Evidence and Explanation - a Reply to Lee. Zoologica Scripta *31:*221-223.

Buikstra JE (1972) Techniques for Coping with Age Regressive Nature Non-Metric Traits. Abstract. American Journal of Physical Anthropology *37:*431-432.

Buikstra JE (1977) Biocultural Dimensions of Archaeological Study: A Regional Perspective. In RL Blakeley (ed.): Biocultural Adaptation in Prehistoric America. Athens: University of Georgia Press, pp. 67-84.

Buikstra JE, Frankenberg SR, and Konigsberg LW (1990) Skeletal Biological Distance Studies in American Physical Anthropology: Recent Trends. American Journal of Physical Anthropology *82:*1-7.

Buikstra JE, and Ubelaker DH (1994) Standards for Data Collection from Human Skeletal Remains: Proceedings of a Seminar at the Field Museum of Natural History, Organized by Jonathan Haas. Fayetteville: Arkansas Archeological Survey.

Byles RH (1976) Different Rates in the Evolution of Proteins and Phenotypes. Annual Review of Anthropology *5:*69-91.

Chapman R, Kinnes I, and Randsborg K (1981) The Archaeology of Death. Cambridge: Cambridge University Press.

Churchill SE, and Smith FH (2000) Makers of the Early Aurignacian of Europe. Yearbook of Physical Anthropology *43:*61-115.

Collard M, and Wood B (2000) How Reliable Are Human Phylogenetic Hypotheses? Proceedings of the National Academy of Sciences *97:*5003-5006.

Conner MD (1990) Population Structure and Skeletal Variation in the Late Woodland. American Journal of Physical Anthropology *82:*31-43.

Coon CS (1963) The Origin of Races. New York: Knopf.

Corruccini RS (1974) An Examination of the Meaning of Cranial Discrete Traits for Human Skeletal Biological Studies. American Journal of Physical Anthropology *40:*425-445.

Corruccini RS (2001) Confidence Intervals for Morphology-Based Cladistic Trees: A Platyrrhine Phylogeny Test Case. International Journal of Primatology *22:*1007-1019.

Cox M (1996) Life and Death in Spitalfields 1700 to 1850. York: Council for British Archaeology.

Cracraft J (1974) Phylogenetic Models and Classification. Systematic Zoology *23:*71-90.

Cracraft J (1978) Science, Philosophy, and Systematics. Systematic Zoology *27:*216-218.

Cracraft J (1982) Phylogenetic Relationships and Monophyly of Loons, Grebes, and Hesperornithiform Birds, with Comments on the Early History of Birds. Systematic Zoology *31:*35-56.

Donlon DA (2000) The Value of Infracranial Nonmetric Variation in Studies of Modern *Homo sapien*s: An Australian Focus. American Journal of Physical Anthropology *113:*349-368.

Edwards JG (1954) A New Approach to Infraspecific Categories. Systematic Zoology *3:*1-20.

Eldredge N, and Cracraft J (1980) Phylogenetic Patterns and the Evolutionary Process: Method and Theory in Comparative Biology. New York: Columbia University Press.

Engelmann GF, and Wiley EO (1977) The Place of Ancestor-Descendant Relationships in Phylogeny Reconstruction. Systematic Zoology *26:*1-11.

Farris JS (1971) The Hypothesis of Nonspecificity and Taxonomic Congruence. Annual Review of Ecology and Systematics *2:*277-302.

Farris JS, and Kluge AG (1986) Synapomorphy, Parsimony, and Evidence. Taxon *35:*298-306.

Finnegan M (1978) Non-Metric Variation of the Infracranial Skeleton. Journal of Anatomy *125:*23-27.

Finnegan M (1984) Multivariate Distances and Multivariate Classification Systems Using Non-Metric Traits in Biological Studies. In GN van Vark and WW Howells (eds.): Multivariate Statistical Analytical Methods in Physical Anthropology. Drodrecht: D. Reidel Publishing company, pp. 69-80.

Fisher RA (1930) The Genetical Theory of Natural Selection. Oxford: Clarendon Press.

Forey PL (1982) Neontological Analysis Versus Paleontological Stories. In KA Joysey and AE Friday (eds.): Problems of Phylogenetic Reconstruction. London: Academic Press, pp. 119-157.

Fortey RA, and Jefferies RPS (1982) Fossils and Phylogeny - a Compromise Approach. In KA Joysey and AE Friday (eds.): Problems of Phylogenetic Reconstruction. London: Academic Press.

Frost DR, and Kluge AG (1994) A Consideration of Epistemology in Systematic Biology, with Special Reference to Species. Cladistics *10:*259-294.

Funk VA (2001) Ssz 1970-1989: A View of the Years of Conflict. Systematic Biology *50:*153-155.

Gaffney ES (1979) An Introduction to the Logic of Phylogeny Reconstruction. In J Cracraft and N Eldredge (eds.): Phylogenetic Analysis and Paleontology. New York: Columbia University Press, pp. 79-111.

Gehring WJ (1998) Master Control Genes in Development and Evolution: The Homeobox Story. New Haven: Yale University Press.

Genovés S (1967) Proportionality of Long Bones and Their Relation to Stature among Mesoamericans. American Journal of Physical Anthropology *26:*67-77.

Gerhart J, and Kirschner M (1998) Cells, Embryos, and Evolution. Oxford: Blackwell Science.

Gilbert SF, and Bolker JA (2001) Homologies of Process and Modular Elements of Embryonic Construction. In G Wagner (ed.): The Character Concept in Evolutionary Biology. New York: Academic Press.

Giles E, and Elliot O (1962) Race Identification from Cranial Measurements. Journal of Forensic Sciences *7:*147-157.

Goldstein PZ, and DeSalle R (2000) Phylogenetic Species, Nested Hierarchies, and Character Fixation. Cladistics *16:*364-384.

Gould SJ (1977) Ontogeny and Phylogeny. Cambridge: Belknap Press.

Gould SJ, and Eldredge N (1977) Punctuated Equilibria: The Tempo and Mode of Evolution Reconsidered. Paleobiology *3:*115-151.

Grant T, and Kluge AG (2003) Data Exploration in Phylogenetic Inference: Scientific, Heuristic, or Neither. Cladistics *19:*379-418.

Grüneberg H (1943) The Genetics of the Mouse. Cambridge: Cambridge University Press.

Grüneberg H (1950a) Genetical Studies on the Skeleton of the Mouse I: Minor Variations of the Vertebral Column. Journal of Genetics *50:*112-141.

Grüneberg H (1950b) Genetical Studies on the Skeleton of the Mouse II: Undulated and Its "Modifiers". Journal of Genetics *50:*142-173.

Grüneberg H (1952) Genetical Studies on the Skeleton of the Mouse IV: Quasi-Continuous Variations. Journal of Genetics *51:*95-114.

Grüneberg H (1963) The Pathology of Development: A Study of Inherited Skeletal Disorders in Animals. New York: Wiley.

Haeckel E (1896) The Evolution of Man. New York: D. Appleton and Company.

Hagelberg E (2003) Recombination or Mutation Rate Heterogeneity? Implications for Mitochondrial Eve. Trends in Genetics *19:*84-90.

Hagelberg E, Goldman N, Lio P, Whelan S, Schiefenhovel W, Clegg J, and Bowden D (1999) Evidence for Mitochondrial DNA Recombination in a Human Population of Island Melanesia. Proceedings of the Royal Society of London Series B *266:*485-492.

Haldane JBS (1932) The Causes of Evolution. New York: Harper and Brothers.

Hall BK (1994) Introduction. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press, pp. 1-19.

Hanihara T, and Ishida H (2001a) Frequency Variations of Discrete Cranial Traits in Major Human Populations. II. Hypostotic Variations. Journal of Anatomy *198:*707-725.

Hanihara T, and Ishida H (2001b) Frequency Variations of Discrete Cranial Traits in Major Human Populations. III. Hyperostotic Variations. Journal of Anatomy *199:*251-272.

Hanihara T, and Ishida H (2001c) Frequency Variations of Discrete Cranial Traits in Major Human Populations. IV. Vessel and Nerve Related Variations. Journal of Anatomy *199:*273-287.

Hanihara T, Ishida H, and Dodo Y (2003) Characterization of Biological Diversity through Analysis of Discrete Cranial Traits. American Journal of Physical Anthropology *121:*241-251.

Hauser G, and De Stefano GF (1989) Epigenetic Variants of the Human Skull. Stuttgart: E. Schweitzerbart'sche Verlagsbuchandlung.

Hennig W (1966) Phylogenetic Systematics. Urbana: University of Illinois Press.

Hillis DM (1994) Homology in Molecular Biology. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press, pp. 339-368.

Hoppa RD, and FitzGerald CM (1999) From Head to Toe: Integrating Studies from Bones and Teeth in Biological Anthropology. In RD Hoppa and CM FitzGerald (eds.): Human Growth in the Past: Studies from Bones and Teeth. Cambridge: Cambridge University Press, pp. 1-31.

Howells WW (1951) Factors of Human Physique. American Journal of Physical Anthropology *9:*159-191.

Howells WW (1969) The Use of Multivariate Techniques in the Study of Skeletal Populations. American Journal of Physical Anthropology *31:*311-314.

Howells WW (1984) Introduction. In GN van Vark and WW Howells (eds.): Multivariate Statistical Methods in Physical Anthropology. Dordrecht: D. Reidel Publishing Company, pp. 1-11.

Howells WW (1995) Who's Who in Skulls: Ethnic Identification of Crania from Measurements. Cambridge: Peabody Museum of Archaeology and Ethnology. Vol. 82.

Hull DL (1979) The Limits of Cladism. Systematic Zoology *28:*416-440.

Hull DL (1985) Bias and Commitment in Science: Phenetics and Cladistics. Annals of Science *42:*319-338.

Hull DL (1999) The Use and Abuse of Sir Karl Popper. Biology and Philosophy *14:*481-504.

Hume D (1739) Treatise of Human Nature. Oxford: Clarendon Press.

Innan H, and Nordborg M (2002) Recombination or Mutational Hot Spots in Human mtDNA? Molecular Biology and Evolution *19:*1122-1127.

Jenner RA (2003) Unleashing the Force of Cladistics? Metazoan Phylogenies and Hypothesis Testing. Integrative Comparative Biology *43:*207-218.

Kellock WL, and Parsons PL (1970) A Comparison of the Incidence of Minor Nonmetrical Cranial Variants in Australian Aborigines with Those of Melanesia and Polynesia. American Journal of Physical Anthropology *33:*235-239.

Key PJ, and Jantz RL (1990) Statistical Assessment of Population Variability: A Methodological Approach. American Journal of Physical Anthropology *82:*53-59.

Kimura M (1983) The Neutral Theory of Molecular Evolution. Cambridge: Cambridge University Press.

Kirsch T, and Claassen H (2000) Matrix Vesicles Mediate Mineralization of Human Thyroid Cartilage. Calcified Tissue International *66:*292-297.

Kitts DB (1977) Karl Popper, Verifiability, and Systematic Zoology. Systematic Zoology *26:*185-194.

Kluge AG (1997) Testability and the Refutation and Corroboration of Cladistic Hypotheses. Cladistics *13:*81-96.

Kluge AG (1999) The Science of Phylogenetic Systematics: Explanation, Prediction, and Test. Cladistics *15:*429-436.

Kluge AG (2001a) Parsimony with and without Scientific Justification. Cladistics *17:*199-210.

Kluge AG (2001b) Philosophical Conjectures and Their Refutation. Systematic Biology *50:*322-330.

Kluge AG (2003a) On the Deduction of Species Relationships: A Précis. Cladistics *19:*233-239.

Kluge AG (2003b) The Repugnant and the Mature in Phylogenetic Inference: Atemporal Similarity and Historical Identity. Cladistics *19:*356-368.

Kluge AG, and Wolf AJ (1993) Cladistics: What's in a Word? Cladistics *9:*183-199.

Knox EB (1998) The Use of Hierarchies as Organizational Models in Systematics. Biological Journal of the Linnean Society *63:*1-49.

Konigsberg LW, and Buikstra JE (1995) Regional Approaches to the Investigation of Past Human Biocultural Structure. In LA Beck (ed.): Regional Approaches to Mortuary Practices. New York: Plenum Press, pp. 191-220.

Kwachka PB, ed. (1994) Perspectives on the Southeast: Linguistics, Archaeology, and Ethnohistory. Athens: University of Georgia Press.

Lahr MM (1996) The Evolution of Modern Human Diversity. Cambridge: Cambridge University Press.

Larsen CS (1997) Bioarchaeology: Interpreting Behavior from the Human Skeleton. Cambridge: Cambridge University Press.

Lee MSY (2002) Divergent Evolution, Hierarchy and Cladistics. Zoologica Scripta *31:*217-219.

Lovejoy CO, Cohn MJ, Ohman JC, and Meindl RS (1996) The Maka Femur: A Case Study in the Application of Analytical Paradigms Dictated by New Developments in Morphological Ontogeny. American Journal of Physical Anthropology *Supplement 22:*152.

Lovejoy CO, Cohn MJ, and White TD (1999) Morphological Analysis of the Mammalian Postcranium: A Developmental Perspective. Proceedings of the National Academy of Sciences *96:*13247-13252.

Lovejoy CO, Mensforth RP, and Armelagos GJ (1982) Five Decades of Skeletal Biology as Reflected in the *American Journal of Physical Anthropology*. In F Spencer (ed.): A History of North American Physical Anthropology, 1930-1980. New York: Academic Press.

Løvtrup S (1974) Epigenetics. New York: John Wiley and Sons.

Marks J (1994) Blood Will Tell (Won't It?): A Century of Molecular Discourse in Anthropological Systematics. American Journal of Physical Anthropology *94:*59-79.

Mayr E (1969) Principles of Systematic Zoology. New York: McGraw-Hill, Inc.

Mayr E (1970) Populations, Species, and Evolution. Cambridge: Belknap Press.

Mayr E (1982) The Growth of Biological Thought: Diversity, Evolution, and Inheritance. Cambridge: Belknap Press.

Mayr E, and Bock WJ (2002) Classifications and Other Ordering Systems. Journal of Zoological Systematics and Evolutionary Research *40:*169-194.

McLaren SB, Schlitter DA, and Genoways HH (1984) Catalogue of the Recent Scandentia and Primates in the Carnegie Museum of Natural History. Annals of Carnegie Museum *53:*463-525.

Melnick DJ, and Hoelzer GA (1993) What Is mtDNA Good for in the Study of Primate Evolution? Evolutionary Anthropology *2:*2-10.

Molleson T, and Cox M (1993) The Spitalfields Project Volume 2 - the Anthropology: The Middling Sort. York: Council for British Archaeology.

Morton SG (1839) Crania Americana. Philadelphia: Dobson.

Nelson G (1979) Cladistic Analysis and Synthesis: Principle and Definitions, with a Historical Note on Adanson's *Familles des Plantes* (1763-1764). Systematic Zoology *28:*1-21.

Nelson G (1989) Cladistics and Evolutionary Models. Cladistics *5:*275-289.

Nelson G (1994) Homology and Systematics. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press, pp. 101-149.

Neumann GK (1952) Archaeology and Race in the American Indian. In JB Griffin (ed.): Archaeology of the Eastern United States. Chicago: University of Chicago Press, pp. 13-34.

Newman MT, and Snow CE (1942) Preliminary Report on the Skeletal Material from Pickwick Basin, Alabama: An Archeological Survey of Pickwick Basin in the Adjacent Portions of the States of Alabama, Mississippi, and Tennessee. Washington: Smithsonian Institution, pp. 393-507.

O'Higgins P, and Vidarsdottir US (1999) New Approaches to the Quantitative Analysis of Craniofacial Growth and Variation. In RD Hoppa and CM FitzGerald (eds.): Human Growth in the Past: Studies from Bones and Teeth. Cambridge: Cambridge University Press, pp. 128-160.

O'Shea J (1984) Mortuary Variability: An Archaeological Investigation. Orlando: Academic Press.

Ossenberg NS (1970) The Influence of Artificial Cranial Deformation on Discontinuous Morphological Traits. American Journal of Physical Anthropology *33:*357-372.

Panchen AL (1994) Richard Owen and the Concept of Homology. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press, pp. 21-62.

Pardoe C (1991) Isolation and Evolution in Tasmania. Current Anthropology *32:*1-21.

Patterson H (1985) The Recognition Concept of Species: Transvaal Museum Monograph No. 4. Pretoria, pp. 21-29.

Pearson K (1924) On the Coefficient of Racial Likeness. Biometrika *18:*109-117.

Pearson K, and Woo TL (1935) Further Investigations of the Morphometric Characters of the Individual Bones of the Skull. Biometrika *27:*424-465.

Peterson HC (2000) On Statistical Methods for Comparison of Intrasample Morpholometric Variability: Zalavár Revisited. American Journal of Physical Anthropology *113:*79-84.

Phelps DS (1983) Archaeology of the North Carolina Coast and Coastal Plain: Problems and Hypotheses. In MA Mathis and JJ Crow (eds.): The Prehistory of North Carolina: An Archaeological Symposium. Raleigh: North Carolina Division of Archives and History.

Pietrusewsky M (2000) Metric Analysis of Skeletal Remains: Methods and Applications. In MA Katzenberg and SR Saunders (eds.): Biological Anthropology of the Skeleton. New York: Wiley-Liss, pp. 375-415.

Platnick NI (1979) Philosophy and the Transformation of Cladistics. Systematic Zoology *28:*537-546.

Poe S, and Wiens JJ (2000) Character Selection and the Methodology of Morphological Systematics. In JJ Wiens (ed.): Phylogenetic Analysis of Morphological Data. Washington: Smithsonian Institution Press, pp. 20-36.

Popper K (1980) Evolution. New Scientist *87:*611.

Popper K (1983) Realism and the Aim of Science. London: Routledge.

Powell JF, and Neves WA (1999) Craniofacial Morphology of the First Americans: Pattern and Process in the Peopling of the New World. American Journal of Physical Anthropology *42:*153-188.

Pufe T, Mentlein R, Tsokos M, Steven P, Varoga D, Goldring MB, Tillmann BN, and Paulsen FP (2004) VEGF Expression in Adult Permanent Thyroid Cartilage: Implications for Lack of Cartilage Ossification. Bone *35:*543-552.

Raff RA (1996) The Shape of Life: Genes, Development, and the Evolution of Animal Form. Chicago: University of Chicago Press.

Raff RA, and Kaufman TC (1983) Embryos, Genes, and Evolution: The Developmental-Genetic Basis of Evolutionary Change. New York: Macmillan Publishing Co.

Reed JC (1998) The Holladay Site: A Bioarchaeological Analysis of an Ossuary in Horry County, South Carolina. Masters Thesis, University of South Carolina, Columbia.

Reeve J, and Adams M (1993) The Spitalfields Project Volume 1 - the Archaeology: Across the Styx. York: Council for British Archaeology.

Relethford JH (1994) Craniometric Variation among Modern Human Populations. American Journal of Physical Anthropology *95:*53-62.

Richter S, and Meier R (1994) The Development of Phylogenetic Concepts in Hennig's Early Theoretical Publications (1947-1966). Systematic Biology *43:*212-221.

Richtsmeier JT, and McGrath JW (1986) Quantitative Genetics of Cranial Nonmetric Traits in Randombred Mice: Heritability and Etiology. American Journal of Physical Anthropology *69:*51-58.

Rosen DE, Nelson G, and Patterson C (1999) Forward: Illinois Reissue of Phylogenetic Systematics. Urbana: University of Illinois Press, pp. vi-xiii.

Ross AH (2004) Regional Isolation in the Balkan Region: An Analysis of Craniofacial Variation. American Journal of Physical Anthropology *124:*73-80.

Roth VL (1988) The Biological Basis of Homology. In CJ Humphries (ed.): Ontogeny and Systematics. New York: Columbia University Press, pp. 1-26.

Roth VL (1994) Within and between Organisms. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press, pp. 301-337.

Saunders SR (1978) The Development and Distribution of Discontinuous Morphological Variation of the Human Infracranial Skeleton. Ottawa: National Museums of Canada.

Saunders SR (1989) Nonmetric Skeletal Variation. In MY İşcan and KAR Kennedy (eds.): Reconstruction of Life from the Skeleton. New York: Alan R. Liss, pp. 95-108.

Saunders SR, and Popovich F (1978) A Family Study of Two Skeletal Variants: Atlas Bridging and Clinoid Bridging. American Journal of Physical Anthropology *49:*193-204.

Schindler DL (1985) Anthropology in the Arctic: A Critique of Racial Typology and Normative Theory. Current Anthropology *26:*475-500.

Schulting RJ, and Richards MP (2001) Dating Women and Becoming Farmers: New Paleodietary and Ams Dating Evidence from the Breton Mesolithic Cemeteries of Téviec and Hoëdic. Journal of Anthropological Archaeology *20:*314-344.

Schwartz JH (1988) History, Morphology, Paleontology, and Evolution. In JH Schwartz (ed.): Orangutan Biology. New York: Oxford University Press, pp. 69-85.

Schwartz JH (1995) Skeleton Keys: An Introduction to Human Skeletal Morphology, Development, and Analysis. New York: Oxford University Press.

Schwartz JH (1999a) Can We Really Identify Species, Living or Extinct? Anthropologie *37:*211-220.

Schwartz JH (1999b) Homeobox Genes, Fossils, and the Origin of Species. New Anatomist *257:*1-17.

Schwartz JH (1999c) Sudden Origins: Fossils, Genes, and the Emergence of Species. New York: Wiley.

Schwartz JH (2005) Molecular Systematics and Evolution. In RA Meyers (ed.): Encyclopedia of Molecular Cell Biology and Molecular Medicine, 2nd Edition, Volume 8. Weinheim: Wiley-VCH, pp. 515-540.

Schwartz JH, and Brauer J (1990) The Ipiutak Dentition: Implications for Interpreting Sinodonty and Sundadonty. American Journal of Physical Anthropology *81:*292.

Schwartz JH, and Tattersall I (2002) The Human Fossil Record, Vol. 1: Terminology and Craniodental Morphology of the Genus *Homo* (Europe). New York: Wiley-Liss.

Schwartz JH, and Tattersall I (2003) The Human Fossil Record, Vol. 2: Craniodental Morphology of Genus *Homo* (Africa and Asia). New York: Wiley-Liss.

Schwartz JH, and Tattersall I (2005) The Human Fossil Record, Vol. 4: Craniodental Morphology of Early Hominids and Overview. New York: Wiley-Liss.

Sciulli PW (1990) Cranial Metric and Discrete Trait Variation and Biological Differentiation in the Terminal Late Archaic of Ohio: The Duff Site Cemetery. American Journal of Physical Anthropology *82:*19-29.

Scott GR, and Turner II CG (1997) The Anthropology of Modern Human Teeth: Dental Morphology and Its Variation in Recent Human Populations. Cambridge: Cambridge University Press.

Sempowski ML, and Spence MW (1994) Mortuary Practices and Skeletal Remains at Teotihuacán. Salt Lake City: University of Utah Press.

Shubin N, Tabin C, and Carroll S (1997) Fossils, Genes, and the Evolution of Animal Limbs. Nature *388:*639-648.

Siddal ME, and Kluge AG (1997) Probabilism and Phylogenetic Inference. Cladistics *13:*313-336.

Simpson GG (1961) Principles of Animal Taxonomy. New York: Columbia University Press.

Sjøvold T (1973) The Occurrence of Minor, Non-Metrical Variants in the Skeleton and Their Quantitative Treatment for Population Comparisons. Homo *24:*204-233.

Sjøvold T (1977) Non-Metrical Divergence between Skeletal Populations. Ossa *4 Suppl. 1:*1-133.

Sjøvold T (1984) Heritability of Some Cranial Measurements and Non-Metric Traits. In GN van Vark and WW Howells (eds.): Multivariate Statistical Methods on Physical Anthropology. Dordrecht: D. Reidel Publishing Company, pp. 233-246.

Sjøvold T (1995) Testing Assumptions for Skeletal Studies by Means of Identified Skulls from Hallstatt, Austria. In S Saunders and A Herring (eds.): Grave Reflections: Portraying the Past through Cemetery Studies. Toronto: Canadian Scholars' Press.

Smith FH, Simek JF, and Harrill MS (1989) Geographic Variation in Supraorbital Torus Reduction During the Later Pleistocene (C. 80,000-15,000 Bp). In P Mellars and CB Stringer (eds.): The Human Revolution. Princeton: Princeton University Press.

Smith JM, and Smith NH (2002) Recombination in Animal Mitochondrial DNA. Molecular Biology and Evolution *19:*2330-2332.

Sneath PHA, and Sokal RR (1973) Numerical Taxonomy. San Francisco: W. H. Freeman and Co.

Sokal RR (1986) Phenetic Taxonomy: Theory and Methods. Annual Review of Ecology and Systematics *17:*423-442.

Sokal RR (1988) Genetic, Geographic, and Linguistic Distances in Europe. Proceedings of the National Academy of Sciences *85:*1722-1726.

Sokal RR, and Rohlf FJ (1969) Biometry. New York: W. H. Freeman and Co.

Sokal RR, Smouse PE, and Neel JV (1986) The Genetic Structure of a Tribal Population, the Yanomama Indians. Xv. Patterns Inferred by Autocorrelation Analysis. Genetics *114:*259-281.

Sokal RR, and Sneath PHA (1963) Principles of Numerical Taxonomy. San Francisco: W. H. Freeman and Co.

St. Hoyme LE, and İşcan MY (1989) Determination of Sex and Race: Accuracy and Assumptions. In MY İşcan and KAR Kennedy (eds.): Reconstruction of Life from the Skeleton. New York: Alan R. Liss, Inc.

Stewart TD (1979) Essentials of Forensic Anthropology, Especially as Developed in the United States. Springfield, Ill.: Thomas.

Stone AC (2000) Ancient DNA from Skeletal Remains. In MA Katzenberg and SR Saunders (eds.): Biological Anthropology of the Human Skeleton. New york: Wiley-Liss, pp. 351-371.

Stoneking M (2000) Hypervariable Sites in the mtDNA Control Region Are Mutational Hotspots. American Journal of Human Genetics *67:*1029-1032.

Stringer CB (2001) Modern Human Origins - Distinguishing the Models. African Archaeological Review *18:*67-75.

Stringer CB, Humphrey LT, and Compton T (1997) Cladistic Analysis of Dental Traits in Recent Humans Using a Fossil Outgroup. Journal of Human Evolution *32:*389-402.

Stump DP (2005) Taxonomy of the Genus *Perodicticus*. Ph.D. Dissertation, University of Pittsburgh, Pittsburgh.

Szathmary EJE (1985) Comments On "Anthropology in the Arctic: A Critique of Racial Typology and Normative Theory". Current Anthropology *26:*489-490.

Tattersall I (1997) Out of Africa Again...and Again? Scientific American *276:*60-67.

Tattersall I, and Schwartz JH (2000) Extinct Humans. Boulder: Westview Press.

Thain M, and Hickman M (1994) The Penguin Dictionary of Biology, Ninth Ed. London: Penguin Books.

Thiele K (1993) The Holy Grail of the Perfect Character: The Cladistic Treatment of Morphometric Data. Cladistics *9:*275-304.

Thorne AG, and Wolpoff MH (1981) Regional Continuity in Australasian Pleistocene Hominid Evolution. American Journal of Physical Anthropology *55:*337-349.

Thorne AG, and Wolpoff MH (1992) The Multiregional Evolution of Modern Humans. Scientific American *266:*76-83.

Thorogood P (1997) The Genotype/Phenotype Relationship. In P Throrogood (ed.): Embryos, Genes, and Birth Defects. New York: John Wiley, pp. 1-11.

Trinkaus E (1978) Bilateral Asymmetry of Human Skeletal Non-Metric Traits. American Journal of Physical Anthropology *49:*315-318.

Turner II CG (1990) Major Features of Sundadonty and Sinodonty, Including Suggestions About East Asian Microevolution, Population History, and Late Pleistocene Relationships with Australian Aboriginals. American Journal of Physical Anthropology *82:*295-317.

Turner II CG (1992) The Dental Bridge between Australia and Asia: Following Macintosh into the East Asian Hearth of Humanity. Archaeologica Oceania *27:*143-152.

Tyrrell A (2000) Skeletal Nonmetric Traits and the Assessment of Inter- and Intra-Population Diversity: Past Problems and Future Potential. In M Cox and S Mays (eds.): Human Osteology in Archaeology and Forensic Science. London: Greenwich Medical Media, pp. 289-306.

Ubelaker DH (1989) Human Skeletal Remains: Excavation, Analysis, Interpretation. Washington, D.C.: Taraxacum.

Valentine JW (2004) On the Origin of Phyla. Chicago: The University of Chicago Press.

van Vark GN, and Howells WW, eds. (1984) Multivariate Statistical Methods in Physical Anthropology. Dordrecht: D. Reidel Publishing Company.

Viguier B (2002) Is the Morphological Disparity of Lemur Skulls (Primates) Controlled by Phylogeny and/or Environmental Constraints? Biological Journal of the Linnean Society *76:*577-590.

Waddington CH (1960) Organisers and Genes. London: Cambridge University Press.

Wagner GP (1989) The Biological Homology Concept. Annual Review of Ecological Systematics *20:*51-69.

Wagner GP (1994) Homology and the Mechanisms of Development. In BK Hall (ed.): Homology: The Hierarchical Basis of Comparative Biology. San Diego: Academic Press.

Weidenreich F (1946) Apes, Giants and Man. Chicago: University of Chicago Press.

Weiss KM (1985) Comments On "Anthropology in the Arctic: A Critique of Racial Typology and Normative Theory" By Debra L. Schindler. Current Anthropology *26:*490-491.

Weiss KM (1993) A Tooth, a Toe and a Vertebra: The Genetic Dimensions of Complex Morphological Traits. Evolutionary Anthropology *2:*121-134.

Weiss KM, and Chakraborty R (1982) Genes, Populations, and Disease, 1930-1980: A Problem-Oriented Review. In F Spencer (ed.): A History of American Physical Anthropology, 1930-1980. New York: Academic Press, pp. 371-404.

Wiens JJ (1999) Polymorphism in Systematics and Comparative Biology. Annual Review of Ecological Systematics *30:*327-362.

Wilmink FW, and Uytterschaut HT (1984) Cluster Analysis, History, Theory and Applications. In GN van Vark and WW Howells (eds.): Multivariate Statistical Methods in Physical Anthropology. Dordrecht: D. Reidel Publishing Company, pp. 135-175.

Wolpoff MH (1989) Multiregional Evolution: The Fossil Alternative to Eden. In P Mellars and CB Stringer (eds.): The Human Revolution: Behavioral and Biological Perspectives on the Origins of Modern Humans. Princeton: Princeton University Press, pp. 62-108.

Wolpoff MH, Hawkes J, and Caspari R (2000) Multiregional, Not Multiple, Origins. American Journal of Physical Anthropology *112:*129-136.

Wolpoff MH, Wu XZ, and Thorne AG (1984) Modern *Homo sapiens* Origins: A General Theory of Hominid Evolution Involving Fossil Evidence from East Asia. In FH Smith and F Spencer (eds.): The Origin of Modern Humans: A World Survey of the Fossil Evidence. New York: Alan R. Liss, pp. 411-483.

Wood B (2005) Review of *the Human Fossil Record, Vol. 2*. Quarterly Review of Biology *80:*105-107.

Wright S (1923) The Duchess Family of Shorthorns as Bred by Thomas Bates. Journal of Heredity *14:*405-422.

Wright S (1939) Statistical Genetics in Relation to Evolution. Paris: Hermann and Cie.

Wright S (1978) The Relation of Livestock Breeding to Theories of Evolution. Journal of Animal Science *46:*1192-1200.